MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:51:23 1998; MasPar time 9.06 Seconds
664.722 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 40.352; Variance 65.917; scale 0.612

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1023	94.9	207	2	Q16528	VEGF RELATED FACTOR IS	1.25e-224
2	947	87.8	207	10	Q64290	VASCULAR ENDOTHELIAL G	3.22e-205
3	620	57.5	116	10	O35485	VASCULAR ENDOTHELIAL G	1.25e-122
4	395	36.6	148	12	O42571	VASCULAR ENDOTHELIAL G	1.95e-67
5	373	34.6	232	2	Q16889	VASCULAR ENDOTHELIAL G	3.57e-62
6	369	34.2	194	12	O42572	VASCULAR ENDOTHELIAL G	3.20e-61
7	333	30.9	216	12	Q91420	VASCULAR ENDOTHELIAL G	1.06e-52
8	278	25.8	75	4	O18843	VASCULAR ENDOTHELIAL G	6.32e-40
9	275	25.5	158	10	Q63434	PLACENTA GROWTH FACTOR	3.07e-39
10	198	18.4	358	10	P97946	VASCULAR ENDOTHELIAL G	4.03e-22
11	192	17.8	326	10	O35251	VASCULAR ENDOTHELIAL G	7.71e-21
12	176	16.3	415	10	P97953	VASCULAR ENDOTHELIAL G	1.80e-17
13	170	15.8	185	2	Q15354	C-SIS PROTO-ONCOGENE (	3.14e-16
14	170	15.8	271	11	O41283	POLYPROTEIN PRECURSOR	3.14e-16
15	168	15.6	210	4	Q29613	C-SIS ONCOGENE (PLATEL	8.10e-16
16	147	13.6	183	10	Q63740	PDGF PROTEIN (FRAGMENT	1.37e-11
17	118	10.9	126	10	O35757	VASCULAR ENDOTHELIAL G	4.18e-06
18	97	9.0	952	9	O32915	GLYCINE DEHYDROGENASE	1.71e-02
19	93	8.6	411	8	Q38946	GLUTAMATE DEHYDROGENAS	7.48e-02
20	89	8.3	571	9	Q51763	IS1162 DNA.	3.15e-01
21	87	8.1	411	8	O04937	NADH GLUTAMATE DEHYDRO	6.35e-01
22	86	8.0	394	9	P96447	EXPA6.	8.98e-01
23	86	8.0	605	2	O00304	VOLTAGE-DEPENDENT CALC	8.98e-01
24	85	7.9	411	8	O04871	GLUTAMATE DEHYDROGENAS	1.27e+00
25	85	7.9	411	8	Q43260	GLUTAMATE DEHYDROGENAS	1.27e+00
26	85	7.9	411	8	O04872	GLUTAMATE DEHYDROGENAS	1.27e+00
27	85	7.9	412	8	P93541	GLUTAMATE DEHYDROGENAS	1.27e+00
28	85	7.9	423	10	P97569	KALLISTATIN.	1.27e+00
29	84	7.8	641	10	Q08463	FRIZZLED PROTEIN HOMOL	1.78e+00
30	83	7.7	393	9	Q46412	MAJOR OUTER MEMBRANE P	2.49e+00
31	83	7.7	393	9	Q46413	(INDIVIDUAL ISOLATE 11	2.49e+00
32	83	7.7	393	9	Q46411	(INDIVIDUAL ISOLATE 98	2.49e+00
33	83	7.7	393	9	Q46414	MAJOR OUTER MEMBRANE P	2.49e+00
34	83	7.7	393	9	Q46415	MAJOR OUTER MEMBRANE P	2.49e+00
35	83	7.7	393	9	Q46410	MAJOR OUTER MEMBRANE P	2.49e+00
36	83	7.7	393	9	Q46409	MAJOR OUTER MEMBRANE P	2.49e+00
37	83	7.7	394	9	O06020	MAJOR OUTER MEMBRANE P	2.49e+00
38	83	7.7	394	9	Q46408	MAJOR OUTER MEMBRANE P	2.49e+00
39	83	7.7	396	9	Q46406	MAJOR OUTER MEMBRANE P	2.49e+00
40	83	7.7	722	3	Q19738	F22E12.1 (FRAGMENT).	2.49e+00
41	83	7.7	1031	3	O09489	ORGANELLE-TYPE CALCIUM	2.49e+00
42	83	7.7	4096	2	Q13327	DNA DEPENDENT PROTEIN	2.49e+00
43	83	7.7	4127	2	P78527	DNA-DEPENDENT PROTEIN	2.49e+00
44	82	7.6	488	11	Q03822	ENV POLYPROTEIN (CONTA	3.48e+00
45	82	7.6	619	10	Q62309	TESTIS NUCLEAR RNA-BIN	3.48e+00

ALIGNMENTS

RESULT 1
ID Q16528 PRELIMINARY; PRT; 207 AA.
AC Q16528;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.
GN VRF OR VEGF-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
RA HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96325041.
RA OLOFSSON B., PAJUSOLA K., VON EULER G., CHILOV D., ALITALO K.,
RA ERIKSSON U.;
RL J. BIOL. CHEM. 271:19310-19317(1996).
DR EMBL; U43368; G1216396; -.
DR EMBL; U52819; G1488259; -.
DR PROSITE; PS00249; PDGF; 1.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 207 VEGF RELATED FACTOR ISOFORM VRF186.
SQ SEQUENCE 207 AA; 21602 MW; 16BDF6F1 CRC32;

Query Match 94.9%; Score 1023; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.25e-224;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:50:48 1998; MasPar time 5.20 Seconds
689.290 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 42.257; Variance 63.671; scale 0.664

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1023	94.9	188	1	VEGB_HUMAN	VASCULAR ENDOTHELIAL G	3.01e-242
2	947	87.8	188	1	VEGB_MOUSE	VASCULAR ENDOTHELIAL G	3.02e-221
3	383	35.5	146	1	VEGF_SHEEP	VASCULAR ENDOTHELIAL G	2.76e-69
4	375	34.8	190	1	VEGF_RAT	VASCULAR ENDOTHELIAL G	3.16e-67
5	373	34.6	214	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	1.03e-66
6	373	34.6	215	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	1.03e-66
7	371	34.4	190	1	VEGF_PIG	VASCULAR ENDOTHELIAL G	3.37e-66
8	365	33.9	190	1	VEGF_BOVIN	VASCULAR ENDOTHELIAL G	1.16e-64
9	354	32.8	164	1	VEGF_CAVPO	VASCULAR ENDOTHELIAL G	7.56e-62
10	309	28.7	170	1	PLGF_HUMAN	PLACENTA GROWTH FACTOR	1.82e-50
11	303	28.1	133	1	VEGH_ORFN2	VASCULAR ENDOTHELIAL G	5.77e-49
12	282	26.2	158	1	PLGF_MOUSE	PLACENTA GROWTH FACTOR	9.45e-44
13	264	24.5	128	1	VEGF_COTJA	VASCULAR ENDOTHELIAL G	2.48e-39
14	175	16.2	419	1	VEGC_HUMAN	VASCULAR ENDOTHELIAL G	1.81e-18
15	174	16.1	148	1	VEGH_ORFN7	VASCULAR ENDOTHELIAL G	3.02e-18
16	174	16.1	225	1	PDGB_RAT	PLATELET-DERIVED GROWT	3.02e-18
17	171	15.9	213	1	PDGA_RABIT	PLATELET-DERIVED GROWT	1.39e-17
18	170	15.8	226	1	TSIS_SMSAV	PDGF-RELATED TRANSFORM	2.31e-17
19	170	15.8	241	1	PDGB_HUMAN	PLATELET-DERIVED GROWT	2.31e-17
20	168	15.6	241	1	PDGB_MOUSE	PLATELET-DERIVED GROWT	6.34e-17
21	168	15.6	245	1	PDGB_FELCA	PLATELET-DERIVED GROWT	6.34e-17
22	165	15.3	211	1	PDGA_MOUSE	PLATELET-DERIVED GROWT	2.87e-16
23	164	15.2	204	1	PDGA_RAT	PLATELET-DERIVED GROWT	4.74e-16
24	164	15.2	211	1	PDGA_HUMAN	PLATELET-DERIVED GROWT	4.74e-16
25	163	15.1	226	1	PDGA_XENLA	PLATELET-DERIVED GROWT	7.81e-16
26	157	14.6	241	1	PDGB_SHEEP	PLATELET-DERIVED GROWT	1.54e-14
27	91	8.4	411	1	DHE3_VITVI	GLUTAMATE DEHYDROGENAS	8.40e-02
28	91	8.4	493	1	ACHE_HUMAN	ACETYLCHOLINE RECEPTOR	8.40e-02
29	90	8.3	539	1	LI14_CAEEL	LIN-14 PROTEIN.	1.22e-01
30	88	8.2	598	1	CYSJ_SALTY	SULFITE REDUCTASE (NAD	2.55e-01
31	87	8.1	411	1	LYOX_MOUSE	PROTEIN-LYSINE 6-OXIDA	3.67e-01
32	86	8.0	567	1	CCB2_HUMAN	DIHYDROPYRIDINE-SENSIT	5.26e-01
33	86	8.0	649	1	YAY3_SCHPO	HYPOTHETICAL 74.5 KD P	5.26e-01
34	85	7.9	60	1	MT3_PICGL	METALLOTHIONEIN-LIKE P	7.51e-01
35	84	7.8	916	1	SCRB_LIMPO	BETA SCRUIN.	1.07e+00
36	84	7.8	941	1	GCSP_MYCTU	PROBABLE GLYCINE DEHYD	1.07e+00
37	83	7.7	174	1	YY19_HUMAN	HYPOTHETICAL Y-CHROMOS	1.52e+00
38	83	7.7	393	1	OMPL_CHLTR	MAJOR OUTER MEMBRANE P	1.52e+00
39	83	7.7	394	1	OMPB_CHLTR	MAJOR OUTER MEMBRANE P	1.52e+00
40	83	7.7	395	1	OMPF_CHLTR	MAJOR OUTER MEMBRANE P	1.52e+00
41	83	7.7	396	1	OMPA_CHLTR	MAJOR OUTER MEMBRANE P	1.52e+00
42	83	7.7	397	1	OMPN_CHLTR	MAJOR OUTER MEMBRANE P	1.52e+00
43	83	7.7	399	1	P2X1_RAT	P2X PURINOCEPTOR 1 (AT	1.52e+00
44	83	7.7	601	1	PDM1_DROME	NUBBIN PROTEIN (TWAIN	1.52e+00
45	83	7.7	1110	1	VGLM_INSV	M POLYPROTEIN PRECURSO	1.52e+00

ALIGNMENTS

RESULT 1
ID VEGB_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE FACTOR).
GN VEGFB OR VRF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96197355.
RA OLOFSSON B., PAJUSOLA K., KAIPAINEN A., VON EULER G., JOUKOV V.,
RA SAKSELA O., ORPANA A., PETTERSSON R.F., ALITALO K., ERIKSSON U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,
RA WARD L., HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL; U48801; G1234823; -.
DR EMBL; U43369; G1216398; -.
DR MIM; 601398; -.
DR PROSITE; PS00249; PDGF; 1.
KW MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21261 MW; 35EA8904 CRC32;

Query Match 94.9%; Score 1023; DB 1; Length 188;
Best Local Similarity 97.9%; Pred. No. 3.01e-242;
Matches 138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:49:30 1998; MasPar time 7.64 Seconds
684.018 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 40.311; Variance 76.368; scale 0.528

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	947	87.8	188	2	JC4680	vascular endothelial	9.64e-177
2	947	87.8	207	2	JC4679	vascular endothelial	9.64e-177
3	383	35.5	146	2	S57956	ovine vascular endoth	2.14e-55
4	375	34.8	120	2	A33787	vascular endothelial	9.54e-54
5	375	34.8	190	2	A35987	glioma-derived vascul	9.54e-54
6	373	34.6	214	2	A44881	vascular endothelial	2.46e-53
7	373	34.6	232	2	A41551	vascular endothelial	2.46e-53
8	371	34.4	190	2	S52130	vascular endothelial	6.35e-53
9	371	34.4	190	2	B44881	vascular endothelial	6.35e-53
10	365	33.9	190	2	B40080	vascular endothelial	1.09e-51
11	318	29.5	149	2	A41236	placental growth fact	4.01e-42
12	302	28.0	133	2	B49530	vascular endothelial	6.60e-39
13	275	25.5	158	2	A56125	placental growth fact	1.55e-33
14	264	24.5	128	2	I51295	vascular endothelial	2.27e-31
15	175	16.2	419	2	S69207	vascular endothelial	1.50e-14
16	174	16.1	148	2	D49530	16K vascular endothel	2.26e-14
17	174	16.1	225	2	S25097	platelet-derived grow	2.26e-14
18	171	15.9	166	2	JN0248	platelet-derived grow	7.79e-14
19	171	15.9	198	2	JS0735	platelet-derived grow	7.79e-14
20	170	15.8	161	2	I38108	platelet-derived grow	1.17e-13
21	170	15.8	185	2	S58383	hypothetical protein	1.17e-13
22	170	15.8	226	1	TVMVSS	PDGF-related transfor	1.17e-13
23	170	15.8	230	2	A55030	platelet-derived grow	1.17e-13
24	170	15.8	241	1	PFHUG2	platelet-derived grow	1.17e-13
25	168	15.6	241	1	PFMSGB	platelet-derived grow	2.66e-13
26	168	15.6	245	1	TVCTSS	platelet-derived grow	2.66e-13
27	164	15.2	196	2	B28964	platelet-derived grow	1.36e-12
28	164	15.2	197	2	S25096	platelet-derived grow	1.36e-12
29	164	15.2	211	1	PFHUG1	platelet-derived grow	1.36e-12
30	163	15.1	200	2	I51551	platelet-derived grow	2.04e-12
31	163	15.1	215	2	S08220	platelet-derived grow	2.04e-12
32	163	15.1	226	2	I51550	platelet-derived grow	2.04e-12
33	161	14.9	196	2	A37359	platelet-derived grow	4.58e-12
34	156	14.5	271	2	A25669	PDGF-related transfor	3.41e-11
35	153	14.2	63	5	1PDGB2	Platelet-derived grow	1.13e-10
36	153	14.2	66	5	1PDGC2	Platelet-derived grow	1.13e-10
37	153	14.2	68	5	1PDGA2	Platelet-derived grow	1.13e-10
38	145	13.5	196	2	A48851	platelet-derived grow	2.64e-09
39	91	8.4	36	2	A60706	vascular endothelial	6.23e-01
40	91	8.4	411	2	S54797	glutamate dehydrogena	6.23e-01
41	91	8.4	493	2	S34775	nicotinic acetylcholi	6.23e-01
42	90	8.3	537	2	B40581	embryonic nuclear pro	8.51e-01
43	90	8.3	539	2	A40581	embryonic nuclear pro	8.51e-01
44	88	8.2	599	2	A34231	sulfite reductase (NA	1.57e+00
45	88	8.2	604	2	A42044	beta subunit of L-typ	1.57e+00

ALIGNMENTS

```
RESULT    1
ENTRY             JC4680     #type complete
TITLE             vascular endothelial growth factor-related factor 167 - mouse
ALTERNATE_NAMES   VRF 167 protein
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              10-May-1996 #sequence_revision 19-Jul-1996 #text_change
                    10-Sep-1997
ACCESSIONS        JC4680
REFERENCE         JC4679
   #authors       Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
                    Nordenskjoeld, M.; Weber, G.; Hayward, N.
   #journal       Biochem. Biophys. Res. Commun. (1996) 220:922-928
   #title         Characterization of the murine VEGF-related factor gene.
   #accession     JC4680
      ##molecule_type mRNA
      ##residues       1-188 ##label TOW
      ##cross-references GB:U43837; NID:g1314335; PID:g1314336
COMMENT     This factor is a mitogen, that is selective for endothelial cells,
            and belongs to a family of growth factor. This transcript is
            differentially spliced to produce two major isoforms, vascular
            endothelial growth factors 167 and VEGF 186.
GENETICS
   #gene          vrf
   #map_position 19
   #introns       137/2
FEATURE
   1-21                #domain signal sequence #status predicted #label SIG\
   22-188              #product vascular endothelial growth factor-related
                         factor #status predicted #label MAT
SUMMARY           #length 188  #molecular-weight 21442  #checksum 5881

  Query Match           87.8%;  Score 947;  DB 2;  Length 188;
  Best Local Similarity  87.2%;  Pred. No. 9.64e-177;
  Matches   123;  Conservative   10;  Mismatches   8;  Indels   0;  Gaps   0;

Db       1 MSPLLRRLLLVALLQLARTQAPVSQFDGPSHQKKVVPWIDVYARATCQPREVVVPLSMEL 60
           |||||||||| |||||| :|||||| |:|:||:|||:|||||:|||||||||||||::||
Qy       1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

Db      61 MGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIQYPSSQLGEMSLEEHS 120
           || | ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy      61 MGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIRYPSSQLGEMSLEEHS 120

Db     121 QCECRPKKKESAVKPDSPRIL 141
           |||||||||:|||||| | |
Qy     121 QCECRPKKKDSAVKPDRCRKL 141
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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:53:16 1998; MasPar time 9.07 Seconds
498.946 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 288199 seqs, 31643258 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP
17:NEWU6 18:NEWU7 19:NEWU8 20:NEWU9

Statistics: Mean 29.808; Variance 121.862; scale 0.245

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1023	94.9	188	9	US-	Sequence 11, Applicati	6.14e-92
2	1023	94.9	188	10	US-	Sequence 11, Applicati	6.14e-92
3	1023	94.9	188	10	US-	Sequence 11, Applicati	6.14e-92
4	1023	94.9	188	8	US-	Sequence 11, Applicati	6.14e-92
5	1023	94.9	188	11	US-	Sequence 57, Applicati	6.14e-92
6	1023	94.9	188	10	US-	Sequence 56, Applicati	6.14e-92
7	1023	94.9	188	9	US-	Sequence 11, Applicati	6.14e-92
8	1023	94.9	188	9	US-	Sequence 11, Applicati	6.14e-92
9	1023	94.9	207	9	US-	Sequence 15, Applicati	6.14e-92
10	1023	94.9	207	10	US-	Sequence 15, Applicati	6.14e-92
11	1023	94.9	207	9	US-	Sequence 15, Applicati	6.14e-92
12	1023	94.9	207	10	US-	Sequence 15, Applicati	6.14e-92
13	1023	94.9	207	9	US-	Sequence 15, Applicati	6.14e-92
14	1005	93.2	206	12	US-	Sequence 2, Applicatio	4.49e-90
15	950	88.1	188	12	US-	Sequence 1, Applicatio	2.19e-84
16	947	87.8	188	8	US-	Sequence 5, Applicatio	4.48e-84
17	947	87.8	188	10	US-	Sequence 5, Applicatio	4.48e-84
18	947	87.8	188	9	US-	Sequence 5, Applicatio	4.48e-84
19	947	87.8	188	8	US-	Sequence 5, Applicatio	4.48e-84
20	947	87.8	188	9	US-	Sequence 5, Applicatio	4.48e-84
21	947	87.8	188	9	US-	Sequence 5, Applicatio	4.48e-84
22	947	87.8	188	10	US-	Sequence 5, Applicatio	4.48e-84
23	945	87.7	207	9	US-	Sequence 13, Applicati	7.21e-84
24	945	87.7	207	10	US-	Sequence 13, Applicati	7.21e-84
25	945	87.7	207	10	US-	Sequence 13, Applicati	7.21e-84
26	945	87.7	207	9	US-	Sequence 13, Applicati	7.21e-84
27	945	87.7	207	9	US-	Sequence 13, Applicati	7.21e-84
28	899	83.4	221	14	US-	Sequence 2, Applicatio	4.06e-79
29	899	83.4	221	8	US-	Sequence 2, Applicatio	4.06e-79
30	899	83.4	221	8	US-	Sequence 2, Applicatio	4.06e-79
31	897	83.2	133	8	US-	Sequence 9, Applicatio	6.54e-79
32	897	83.2	133	10	US-	Sequence 9, Applicatio	6.54e-79
33	897	83.2	133	9	US-	Sequence 9, Applicatio	6.54e-79
34	897	83.2	133	8	US-	Sequence 9, Applicatio	6.54e-79
35	897	83.2	133	9	US-	Sequence 9, Applicatio	6.54e-79
36	897	83.2	133	10	US-	Sequence 9, Applicatio	6.54e-79
37	897	83.2	133	9	US-	Sequence 9, Applicatio	6.54e-79
38	891	82.7	221	12	US-	Sequence 5, Applicatio	2.72e-78
39	870	80.7	195	9	US-	Sequence 7, Applicatio	3.99e-76
40	870	80.7	195	9	US-	Sequence 7, Applicatio	3.99e-76
41	870	80.7	195	10	US-	Sequence 7, Applicatio	3.99e-76
42	870	80.7	195	10	US-	Sequence 7, Applicatio	3.99e-76
43	870	80.7	195	9	US-	Sequence 7, Applicatio	3.99e-76
44	870	80.7	195	8	US-	Sequence 7, Applicatio	3.99e-76
45	870	80.7	195	8	US-	Sequence 7, Applicatio	3.99e-76

ALIGNMENTS

RESULT 1
ID US-08-569-063A-11 STANDARD; PRT; 188 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 11, Application US/08569063A
XX
CC Sequence 11, Application US/08569063A
CC GENERAL INFORMATION:
CC APPLICANT: ERIKSSON, Ulf
CC APPLICANT: OLOFSSON, Birgitta
CC APPLICANT: ALITALO, Kari
CC APPLICANT: PAJUSOLA, Katri
CC TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC TITLE OF INVENTION: DNA CODING THEREFOR
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
CC STREET: 1200 G Street, N.W., Suite 700
CC CITY: Washington
CC STATE: DC
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/569,063A
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/469,427
CC FILING DATE: 06-JUN-1995
CC APPLICATION NUMBER: US 08/397,651
CC FILING DATE: 01-MAR-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: EVANS, Joseph D.
CC REGISTRATION NUMBER: 26,269
CC REFERENCE/DOCKET NUMBER: 41979CP2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 628-8800
CC TELEFAX: (202) 628-8844

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:52:52 1998; MasPar time 2.12 Seconds
475.687 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 28.064; Variance 116.805; scale 0.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1023	94.9	188	1	US-08-469-	Sequence 11, Applicati	1.69e-91
2	947	87.8	188	1	US-08-469-	Sequence 5, Applicatio	9.26e-84
3	897	83.2	133	1	US-08-469-	Sequence 9, Applicatio	1.12e-78
4	870	80.7	195	1	US-08-469-	Sequence 7, Applicatio	6.18e-76
5	709	65.8	102	1	US-08-469-	Sequence 2, Applicatio	1.21e-59
6	400	37.1	121	3	5219739-20	Patent No. 5219739.	8.12e-29
7	400	37.1	121	3	5194596-19	Patent No. 5194596.	8.12e-29
8	379	35.2	231	2	PCT-US96-0	Sequence 10, Applicati	9.28e-27
9	378	35.1	191	3	5332671-4	Patent No. 5332671.	1.16e-26
10	377	35.0	165	3	5219739-19	Patent No. 5219739.	1.46e-26
11	377	35.0	165	3	5194596-18	Patent No. 5194596.	1.46e-26
12	375	34.8	120	3	5219739-9	Patent No. 5219739.	2.28e-26
13	375	34.8	120	3	5194596-9	Patent No. 5194596.	2.28e-26
14	374	34.7	215	3	5219739-22	Patent No. 5219739.	2.86e-26
15	373	34.6	214	3	5240848-11	Patent No. 5240848.	3.58e-26
16	373	34.6	215	3	5240848-7	Patent No. 5240848.	3.58e-26
17	365	33.9	190	3	5332671-3	Patent No. 5332671.	2.17e-25
18	352	32.7	164	3	5219739-18	Patent No. 5219739.	4.01e-24
19	352	32.7	164	3	5219739-17	Patent No. 5219739.	4.01e-24
20	352	32.7	164	3	5194596-17	Patent No. 5194596.	4.01e-24
21	348	32.3	189	1	US-08-469-	Sequence 15, Applicati	9.82e-24
22	318	29.5	149	1	US-08-469-	Sequence 14, Applicati	7.95e-21
23	175	16.2	419	2	PCT-US96-0	Sequence 2, Applicatio	2.29e-07
24	172	16.0	109	1	US-08-094-	Sequence 3, Applicatio	4.28e-07
25	172	16.0	109	1	US-08-094-	Sequence 5, Applicatio	4.28e-07
26	170	15.8	109	3	5498600-3	Patent No. 5498600.	6.49e-07
27	170	15.8	109	1	US-08-094-	Sequence 4, Applicatio	6.49e-07
28	170	15.8	109	1	US-08-094-	Sequence 2, Applicatio	6.49e-07
29	170	15.8	109	2	PCT-US93-0	Sequence 1, Applicatio	6.49e-07
30	170	15.8	109	2	PCT-US91-0	Sequence 18, Applicati	6.49e-07
31	170	15.8	120	3	5428135-2	Patent No. 5428135.	6.49e-07
32	170	15.8	160	1	US-08-094-	Sequence 1, Applicatio	6.49e-07
33	170	15.8	220	3	5175255-4	Patent No. 5175255.	6.49e-07
34	170	15.8	226	3	5498600-2	Patent No. 5498600.	6.49e-07
35	170	15.8	241	3	5194596-15	Patent No. 5194596.	6.49e-07
36	170	15.8	241	3	5175255-2	Patent No. 5175255.	6.49e-07
37	170	15.8	241	3	5175255-8	Patent No. 5175255.	6.49e-07
38	170	15.8	241	3	5219739-15	Patent No. 5219739.	6.49e-07
39	170	15.8	241	2	PCT-US96-0	Sequence 9, Applicatio	6.49e-07
40	170	15.8	241	1	US-08-387-	Sequence 4, Applicatio	6.49e-07
41	170	15.8	282	1	US-08-445-	Sequence 1, Applicatio	6.49e-07
42	168	15.6	241	1	US-08-469-	Sequence 13, Applicati	9.82e-07
43	165	15.3	196	1	US-08-469-	Sequence 12, Applicati	1.83e-06
44	164	15.2	125	2	PCT-US92-0	Sequence 4, Applicatio	2.24e-06
45	164	15.2	196	2	PCT-US96-0	Sequence 8, Applicatio	2.24e-06

ALIGNMENTS

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RESULT    1
ID   US-08-469-427A-11      STANDARD;      PRT;    188 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 11, Application US/08469427A
XX
CC    Sequence 11, Application US/08469427A
CC    Patent No. 5607918
CC     GENERAL INFORMATION:
CC       APPLICANT:  Eriksson, Ulf
CC       APPLICANT:  Olofsson, Birgitta
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Pajusola, Katri
CC       TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC       TITLE OF INVENTION:  DNA CODING THEREFOR
CC       NUMBER OF SEQUENCES:  17
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Evenson, McKeown, Edwards & Lenahan
CC         STREET:  1200 G Street, N.W., Suite 700
CC         CITY:  Washington
CC         STATE:  DC
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/469,427A
CC         FILING DATE:  06-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/397,651
CC         FILING DATE:  01-MAR-1995
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Evans, Joseph D
CC         REGISTRATION NUMBER:  26,269
CC         REFERENCE/DOCKET NUMBER:  41979cp2
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (202) 628-8800
CC         TELEFAX:  (202) 628-8844
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  188 amino acids
```

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:47:38 1998; MasPar time 5.75 Seconds
402.740 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CRPKKKDSAVKPDRCRKLRR 143

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 30.138; Variance 121.083; scale 0.249

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1078	100.0	143	19	W00727	Vascular endothelial	1.31e-99
2	1023	94.9	188	19	W00726	Vascular endothelial	8.25e-94
3	1023	94.9	188	21	W04829	Fibrosarcoma vascular	8.25e-94
4	1023	94.9	207	21	W04831	Vascular endothelial	8.25e-94
5	1023	94.9	207	19	W00725	Vascular endothelial	8.25e-94
6	947	87.8	188	21	W04826	Heart vascular endoth	8.22e-86
7	947	87.8	207	21	W04830	Vascular endothelial	8.22e-86
8	937	86.9	188	19	W00864	Murine VRF167.	9.25e-85
9	937	86.9	207	19	W00863	Murine VRF186.	9.25e-85
10	899	83.4	221	23	W07611	Human vascular endoth	9.06e-81
11	897	83.2	133	21	W04828	Vascular endothelial	1.47e-80
12	870	80.7	195	21	W04827	Heart vascular endoth	1.00e-77
13	749	69.5	101	19	W00728	Vascular endothelial	4.56e-65
14	709	65.8	102	21	W04824	Vascular endothelial	6.74e-61
15	411	38.1	377	18	W00586	SAP-AlaMet-VEGF121.	3.27e-30
16	411	38.1	500	18	W00589	SAP-AlaMet-VEGF121-Gl	3.27e-30
17	411	38.1	506	18	W00588	SAP-AlaMet-VEGF121(Gl	3.27e-30
18	411	38.1	512	18	W00590	SAP-AlaMet-VEGF121(Gl	3.27e-30
19	405	37.6	146	5	R27354	Sequence of vascular	1.32e-29
20	405	37.6	146	4	R22348	Alternative form of V	1.32e-29
21	404	37.5	148	18	R94032	VEGF121 Cys+2.	1.67e-29
22	404	37.5	384	18	R94071	SAP(Gly4Ser)VEGF121.	1.67e-29
23	404	37.5	399	18	W00587	SAP(Gly4Ser)4VEGF121.	1.67e-29
24	404	37.5	514	18	R94073	SAP(Gly4Ser)VEGF121(G	1.67e-29
25	404	37.5	524	18	W00594	SAP(Gly4Ser)2VEGF121(	1.67e-29
26	401	37.2	147	18	R94001	VEGF121.	3.36e-29
27	401	37.2	147	16	R91075	Human vascular endoth	3.36e-29
28	400	37.1	121	7	R42607	Human VEGF-121.	4.24e-29
29	400	37.1	121	3	R11385	Human vascular endoth	4.24e-29
30	395	36.6	148	18	R94031	VEGF121 Cys+4.	1.36e-28
31	390	36.2	595	18	W00595	SAP-GlySer-VEGF165(Gl	4.34e-28
32	388	36.0	421	18	W00584	SAP-AlaMet-VEGF165.	6.91e-28
33	388	36.0	588	18	W00592	SAP-AlaMet-VEGF165-Gl	6.91e-28
34	388	36.0	594	18	W00591	SAP-AlaMet-VEGF165(Gl	6.91e-28
35	388	36.0	600	18	W00593	SAP-AlaMet-VEGF165(Gl	6.91e-28
36	381	35.3	192	18	R94040	VEGF165 Cys+2.	3.51e-27
37	381	35.3	428	18	R94072	SAP(Gly4Ser)VEGF165.	3.51e-27
38	381	35.3	443	18	W00585	SAP(Gly4Ser)4VEGF165.	3.51e-27
39	381	35.3	598	18	R94074	SAP(Gly4Ser)VEGF165(G	3.51e-27
40	381	35.3	612	18	W00596	SAP(Gly4Ser)2VEGF165(	3.51e-27
41	378	35.1	191	27	W38242	Vascular endothelial	7.04e-27
42	378	35.1	191	18	R94002	VEGF165.	7.04e-27
43	378	35.1	191	2	R08002	Human vascular endoth	7.04e-27
44	378	35.1	191	16	R91076	Human vascular endoth	7.04e-27
45	378	35.1	592	27	W38233	VEGF/CPG2 fusion prot	7.04e-27

ALIGNMENTS

RESULT 1
ID W00727 standard; Protein; 143 AA.
AC W00727;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e6+e7.
KW Vascular endothelial growth factor; VEGF; SOM175-e6+e7; neuron;
KW astroglial proliferation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..21
FT /label= Sig_peptide
PN WO9627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI; 96-412774/41.
DR N-PSDB; T33612.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 13; Page 46; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 143 AA;

Query Match 100.0%; Score 1078; DB 19; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.31e-99;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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MPSRCH (TM)

****

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:42:57 1998; MasPar time 10.92 Seconds
724.739 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 41.227; Variance 70.997; scale 0.581

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1014	69.5	207	2	Q16528	VEGF RELATED FACTOR IS	4.54e-210
2	938	64.3	207	10	Q64290	VASCULAR ENDOTHELIAL G	1.12e-191
3	611	41.9	116	10	O35485	VASCULAR ENDOTHELIAL G	1.80e-113
4	497	34.1	194	12	O42572	VASCULAR ENDOTHELIAL G	9.00e-87
5	371	25.4	232	2	Q16889	VASCULAR ENDOTHELIAL G	6.76e-58
6	365	25.0	148	12	O42571	VASCULAR ENDOTHELIAL G	1.52e-56
7	330	22.6	216	12	Q91420	VASCULAR ENDOTHELIAL G	1.02e-48
8	278	19.1	75	4	O18843	VASCULAR ENDOTHELIAL G	2.67e-37
9	268	18.4	158	10	Q63434	PLACENTA GROWTH FACTOR	3.85e-35
10	198	13.6	358	10	P97946	VASCULAR ENDOTHELIAL G	1.78e-20
11	192	13.2	326	10	O35251	VASCULAR ENDOTHELIAL G	2.88e-19
12	188	12.9	415	10	P97953	VASCULAR ENDOTHELIAL G	1.82e-18
13	177	12.1	271	11	O41283	POLYPROTEIN PRECURSOR	2.76e-16
14	170	11.7	185	2	Q15354	C-SIS PROTO-ONCOGENE (	6.45e-15
15	168	11.5	210	4	Q29613	C-SIS ONCOGENE (PLATEL	1.58e-14
16	147	10.1	183	10	Q63740	PDGF PROTEIN (FRAGMENT	1.52e-10
17	128	8.8	126	10	O35757	VASCULAR ENDOTHELIAL G	4.15e-07
18	101	6.9	324	10	Q63199	FAS ANTIGEN PRECURSOR.	1.31e-02
19	99	6.8	749	3	Q23804	SPID PRECURSOR (FRAGME	2.69e-02
20	97	6.7	952	9	O32915	GLYCINE DEHYDROGENASE	5.44e-02
21	95	6.5	292	9	P74446	HYPOTHETICAL 32.3 KD P	1.09e-01
22	94	6.4	180	3	Q99072	GIANT SECRETORY PROTEI	1.54e-01
23	94	6.4	187	3	Q23782	BRC GENE (3'END) IN BA	1.54e-01
24	93	6.4	391	3	Q26258	BR2.2=BALBIANI RING {5	2.17e-01
25	93	6.4	411	8	Q38946	GLUTAMATE DEHYDROGENAS	2.17e-01
26	92	6.3	68	11	Q84667	GENOME, PARTIAL SEQUEN	3.05e-01
27	91	6.2	139	3	O00830	(FRAGMENT).	4.27e-01
28	91	6.2	235	3	Q94441	REPETITIVE DNA IN BALB	4.27e-01
29	90	6.2	240	3	Q23780	BRC GENE PRODUCT (FRAG	5.98e-01
30	89	6.1	571	9	Q51763	IS1162 DNA.	8.33e-01
31	87	6.0	112	8	Q40726	DNA BINDING PROTEIN (F	1.61e+00
32	87	6.0	411	8	O04937	NADH GLUTAMATE DEHYDRO	1.61e+00
33	88	6.0	1260	2	O15047	KIAA0339.	1.16e+00
34	87	6.0	2796	9	Q48926	FATTY ACID SYNTHASE.	1.61e+00
35	86	5.9	105	9	Q60232	INCF PLASMID REPFIB RE	2.22e+00
36	86	5.9	394	9	P96447	EXPA6.	2.22e+00
37	86	5.9	470	3	Q22919	COSMID C37C3.	2.22e+00
38	86	5.9	605	2	O00304	VOLTAGE-DEPENDENT CALC	2.22e+00
39	86	5.9	722	11	P89466	TEGUMENT PROTEIN.	2.22e+00
40	86	5.9	919	4	Q28659	FERTILIN ALPHA SUBUNIT	2.22e+00
41	86	5.9	1704	3	Q94446	220 KDA SILK PROTEIN.	2.22e+00
42	85	5.8	411	8	Q43260	GLUTAMATE DEHYDROGENAS	3.06e+00
43	85	5.8	411	8	O04872	GLUTAMATE DEHYDROGENAS	3.06e+00
44	85	5.8	412	8	P93541	GLUTAMATE DEHYDROGENAS	3.06e+00
45	85	5.8	1269	2	Q13045	FLII (HOMOLOG OF D. ME	3.06e+00

ALIGNMENTS

RESULT 1
ID Q16528 PRELIMINARY; PRT; 207 AA.
AC Q16528;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.
GN VRF OR VEGF-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
RA HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96325041.
RA OLOFSSON B., PAJUSOLA K., VON EULER G., CHILOV D., ALITALO K.,
RA ERIKSSON U.;
RL J. BIOL. CHEM. 271:19310-19317(1996).
DR EMBL; U43368; G1216396; -.
DR EMBL; U52819; G1488259; -.
DR PROSITE; PS00249; PDGF; 1.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 207 VEGF RELATED FACTOR ISOFORM VRF186.
SQ SEQUENCE 207 AA; 21602 MW; 16BDF6F1 CRC32;

Query Match 69.5%; Score 1014; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.54e-210;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:41:41 1998; MasPar time 6.16 Seconds
765.523 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 43.185; Variance 67.718; scale 0.638

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1458	100.0	188	1	VEGB_HUMAN	VASCULAR ENDOTHELIAL G	0.00e+00
2	1317	90.3	188	1	VEGB_MOUSE	VASCULAR ENDOTHELIAL G	0.00e+00
3	513	35.2	190	1	VEGF_RAT	VASCULAR ENDOTHELIAL G	1.45e-98
4	511	35.0	190	1	VEGF_PIG	VASCULAR ENDOTHELIAL G	4.68e-98
5	505	34.6	190	1	VEGF_BOVIN	VASCULAR ENDOTHELIAL G	1.57e-96
6	498	34.2	164	1	VEGF_CAVPO	VASCULAR ENDOTHELIAL G	9.43e-95
7	371	25.4	215	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	5.87e-63
8	369	25.3	146	1	VEGF_SHEEP	VASCULAR ENDOTHELIAL G	1.82e-62
9	369	25.3	214	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	1.82e-62
10	321	22.0	170	1	PLGF_HUMAN	PLACENTA GROWTH FACTOR	9.05e-51
11	296	20.3	133	1	VEGH_ORFN2	VASCULAR ENDOTHELIAL G	8.94e-45
12	275	18.9	158	1	PLGF_MOUSE	PLACENTA GROWTH FACTOR	8.41e-40
13	261	17.9	128	1	VEGF_COTJA	VASCULAR ENDOTHELIAL G	1.60e-36
14	181	12.4	225	1	PDGB_RAT	PLATELET-DERIVED GROWT	1.51e-18
15	178	12.2	419	1	VEGC_HUMAN	VASCULAR ENDOTHELIAL G	6.60e-18
16	177	12.1	226	1	TSIS_SMSAV	PDGF-RELATED TRANSFORM	1.08e-17
17	177	12.1	241	1	PDGB_MOUSE	PLATELET-DERIVED GROWT	1.08e-17
18	177	12.1	241	1	PDGB_HUMAN	PLATELET-DERIVED GROWT	1.08e-17
19	176	12.1	245	1	PDGB_FELCA	PLATELET-DERIVED GROWT	1.76e-17
20	174	11.9	148	1	VEGH_ORFN7	VASCULAR ENDOTHELIAL G	4.66e-17
21	171	11.7	213	1	PDGA_RABIT	PLATELET-DERIVED GROWT	2.00e-16
22	169	11.6	211	1	PDGA_HUMAN	PLATELET-DERIVED GROWT	5.26e-16
23	165	11.3	211	1	PDGA_MOUSE	PLATELET-DERIVED GROWT	3.60e-15
24	164	11.2	204	1	PDGA_RAT	PLATELET-DERIVED GROWT	5.81e-15
25	163	11.2	226	1	PDGA_XENLA	PLATELET-DERIVED GROWT	9.36e-15
26	157	10.8	241	1	PDGB_SHEEP	PLATELET-DERIVED GROWT	1.61e-13
27	107	7.3	3707	1	PGBM_MOUSE	BASEMENT MEMBRANE-SPEC	5.14e-04
28	99	6.8	51	1	HSP1_ALOSE	SPERM PROTAMINE P1.	1.13e-02
29	99	6.8	4393	1	PGBM_HUMAN	BASEMENT MEMBRANE-SPEC	1.13e-02
30	96	6.6	100	1	HSP2_ALOSE	SPERM HISTONE P2 PRECU	3.45e-02
31	96	6.6	327	1	FASA_MOUSE	FASL RECEPTOR PRECURSO	3.45e-02
32	93	6.4	503	1	VE2_HPV21	REGULATORY PROTEIN E2.	1.03e-01
33	94	6.4	769	1	ITB2_HUMAN	CELL SURFACE ADHESION	7.17e-02
34	93	6.4	1380	1	ZMS1_YEAST	ZINC FINGER PROTEIN ZM	1.03e-01
35	90	6.2	381	1	SELP_HUMAN	SELENOPROTEIN P PRECUR	2.99e-01
36	91	6.2	411	1	DHE3_VITVI	GLUTAMATE DEHYDROGENAS	2.10e-01
37	91	6.2	493	1	ACHE_HUMAN	ACETYLCHOLINE RECEPTOR	2.10e-01
38	90	6.2	539	1	LI14_CAEEL	LIN-14 PROTEIN.	2.99e-01
39	90	6.2	1004	1	EPA8_MOUSE	EPHRIN TYPE-A RECEPTOR	2.99e-01
40	91	6.2	1060	1	UAY_EMENI	POSITIVE REGULATOR OF	2.10e-01
41	89	6.1	50	1	HSP1_PONPY	SPERM PROTAMINE P1 (CY	4.25e-01
42	89	6.1	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	4.25e-01
43	88	6.0	50	1	HSP1_MOUSE	SPERM PROTAMINE P1 (CY	6.01e-01
44	88	6.0	504	1	MIG1_YEAST	REGULATORY PROTEIN MIG	6.01e-01
45	88	6.0	598	1	CYSJ_SALTY	SULFITE REDUCTASE (NAD	6.01e-01

ALIGNMENTS

RESULT 1
ID VEGB_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE FACTOR).
GN VEGFB OR VRF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96197355.
RA OLOFSSON B., PAJUSOLA K., KAIPAINEN A., VON EULER G., JOUKOV V.,
RA SAKSELA O., ORPANA A., PETTERSSON R.F., ALITALO K., ERIKSSON U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,
RA WARD L., HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL; U48801; G1234823; -.
DR EMBL; U43369; G1216398; -.
DR MIM; 601398; -.
DR PROSITE; PS00249; PDGF; 1.
KW MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21261 MW; 35EA8904 CRC32;

Query Match 100.0%; Score 1458; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:40:03 1998; MasPar time 9.36 Seconds
734.106 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 41.161; Variance 80.141; scale 0.514

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1317	90.3	188	2	JC4680	vascular endothelial	5.71e-251
2	938	64.3	207	2	JC4679	vascular endothelial	2.15e-169
3	513	35.2	190	2	A35987	glioma-derived vascul	7.43e-80
4	511	35.0	190	2	S52130	vascular endothelial	1.92e-79
5	509	34.9	190	2	B44881	vascular endothelial	4.95e-79
6	505	34.6	190	2	B40080	vascular endothelial	3.30e-78
7	371	25.4	232	2	A41551	vascular endothelial	5.30e-51
8	369	25.3	146	2	S57956	ovine vascular endoth	1.33e-50
9	369	25.3	214	2	A44881	vascular endothelial	1.33e-50
10	361	24.8	120	2	A33787	vascular endothelial	5.22e-49
11	296	20.3	149	2	A41236	placental growth fact	3.10e-36
12	295	20.2	133	2	B49530	vascular endothelial	4.84e-36
13	268	18.4	158	2	A56125	placental growth fact	7.49e-31
14	261	17.9	128	2	I51295	vascular endothelial	1.61e-29
15	181	12.4	225	2	S25097	platelet-derived grow	7.66e-15
16	178	12.2	419	2	S69207	vascular endothelial	2.56e-14
17	177	12.1	161	2	I38108	platelet-derived grow	3.83e-14
18	177	12.1	226	1	TVMVSS	PDGF-related transfor	3.83e-14
19	177	12.1	230	2	A55030	platelet-derived grow	3.83e-14
20	177	12.1	241	1	PFMSGB	platelet-derived grow	3.83e-14
21	177	12.1	241	1	PFHUG2	platelet-derived grow	3.83e-14
22	176	12.1	245	1	TVCTSS	platelet-derived grow	5.72e-14
23	174	11.9	148	2	D49530	16K vascular endothel	1.27e-13
24	171	11.7	166	2	JN0248	platelet-derived grow	4.21e-13
25	170	11.7	185	2	S58383	hypothetical protein	6.26e-13
26	171	11.7	198	2	JS0735	platelet-derived grow	4.21e-13
27	169	11.6	211	1	PFHUG1	platelet-derived grow	9.31e-13
28	165	11.3	215	2	S08220	platelet-derived grow	4.52e-12
29	164	11.2	196	2	B28964	platelet-derived grow	6.69e-12
30	164	11.2	197	2	S25096	platelet-derived grow	6.69e-12
31	163	11.2	200	2	I51551	platelet-derived grow	9.91e-12
32	163	11.2	226	2	I51550	platelet-derived grow	9.91e-12
33	163	11.2	271	2	A25669	PDGF-related transfor	9.91e-12
34	161	11.0	196	2	A37359	platelet-derived grow	2.17e-11
35	153	10.5	63	5	1PDGB2	Platelet-derived grow	4.80e-10
36	153	10.5	66	5	1PDGC2	Platelet-derived grow	4.80e-10
37	153	10.5	68	5	1PDGA2	Platelet-derived grow	4.80e-10
38	145	9.9	196	2	A48851	platelet-derived grow	1.01e-08
39	107	7.3	3707	2	S18252	heparan sulfate prote	7.58e-03
40	101	6.9	324	2	JC2395	Fas antigen - rat	5.33e-02
41	99	6.8	749	2	A45294	Balbiani ring 2.1 - m	1.01e-01
42	99	6.8	4391	2	A38096	perlecan precursor -	1.01e-01
43	96	6.6	100	2	S33338	protamine P2 - red ho	2.58e-01
44	96	6.6	327	2	A46484	apoptosis-mediating m	2.58e-01
45	95	6.5	292	2	S76418	hypothetical protein	3.51e-01

ALIGNMENTS

```
RESULT    1
ENTRY             JC4680     #type complete
TITLE             vascular endothelial growth factor-related factor 167 - mouse
ALTERNATE_NAMES   VRF 167 protein
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              10-May-1996 #sequence_revision 19-Jul-1996 #text_change
                    10-Sep-1997
ACCESSIONS        JC4680
REFERENCE         JC4679
   #authors       Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
                    Nordenskjoeld, M.; Weber, G.; Hayward, N.
   #journal       Biochem. Biophys. Res. Commun. (1996) 220:922-928
   #title         Characterization of the murine VEGF-related factor gene.
   #accession     JC4680
      ##molecule_type mRNA
      ##residues       1-188 ##label TOW
      ##cross-references GB:U43837; NID:g1314335; PID:g1314336
COMMENT     This factor is a mitogen, that is selective for endothelial cells,
              and belongs to a family of growth factor. This transcript is
              differentially spliced to produce two major isoforms, vascular
              endothelial growth factors 167 and VEGF 186.
GENETICS
   #gene          vrf
   #map_position 19
   #introns       137/2
FEATURE
   1-21                #domain signal sequence #status predicted #label SIG\
   22-188              #product vascular endothelial growth factor-related
                         factor #status predicted #label MAT
SUMMARY           #length 188  #molecular-weight 21442  #checksum 5881

  Query Match            90.3%;  Score 1317;  DB 2;  Length 188;
  Best Local Similarity  87.8%;  Pred. No. 5.71e-251;
  Matches   165;  Conservative   14;  Mismatches   9;  Indels   0;  Gaps   0;

Db       1 MSPLLRRLLLVALLQLARTQAPVSQFDGPSHQKKVVPWIDVYARATCQPREVVVPLSMEL 60
           |||||||||| |||||| :|||||| |:|:||:|||:|||||:|||||||||||||::||
Qy       1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

Db      61 MGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIQYPSSQLGEMSLEEHS 120
           || | |||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy      61 MGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIRYPSSQLGEMSLEEHS 120

Db     121 QCECRPKKKESAVKPDSPRILCPPCTQRRQRPDPRTCRCRCRRRRFLHCQGRGLELNPDT 180
           |||||||||:|||||||| ||| |||::|||||||||||||| ||:|||||||||||||
Qy     121 QCECRPKKKDSAVKPDSPRPLCPRCTQHHQRPDPRTCRCRCRRRSFLRCQGRGLELNPDT 180
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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:45:20 1998; MasPar time 10.60 Seconds
561.427 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 288199 seqs, 31643258 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP
17:NEWU6 18:NEWU7 19:NEWU8 20:NEWU9

Statistics: Mean 30.883; Variance 128.491; scale 0.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1458	100.0	188	11	US-[redacted]	Sequence 57, Applicati	2.57e-134
2	1458	100.0	188	9	US-[redacted]	Sequence 11, Applicati	2.57e-134
3	1458	100.0	188	10	US-[redacted]	Sequence 11, Applicati	2.57e-134
4	1458	100.0	188	9	US-[redacted]	Sequence 11, Applicati	2.57e-134
5	1458	100.0	188	10	US-[redacted]	Sequence 56, Applicati	2.57e-134
6	1458	100.0	188	9	US-[redacted]	Sequence 11, Applicati	2.57e-134
7	1458	100.0	188	10	US-[redacted]	Sequence 11, Applicati	2.57e-134
8	1458	100.0	188	8	US-[redacted]	Sequence 11, Applicati	2.57e-134
9	1320	90.5	188	12	US-[redacted]	Sequence 1, Applicatio	3.46e-120
10	1317	90.3	188	10	US-[redacted]	Sequence 5, Applicatio	7.01e-120
11	1317	90.3	188	10	US-[redacted]	Sequence 5, Applicatio	7.01e-120
12	1317	90.3	188	8	US-[redacted]	Sequence 5, Applicatio	7.01e-120
13	1317	90.3	188	9	US-[redacted]	Sequence 5, Applicatio	7.01e-120
14	1317	90.3	188	8	US-[redacted]	Sequence 5, Applicatio	7.01e-120
15	1317	90.3	188	9	US-[redacted]	Sequence 5, Applicatio	7.01e-120
16	1317	90.3	188	9	US-[redacted]	Sequence 5, Applicatio	7.01e-120
17	1240	85.0	195	9	US-[redacted]	Sequence 7, Applicatio	5.19e-112
18	1240	85.0	195	10	US-[redacted]	Sequence 7, Applicatio	5.19e-112
19	1240	85.0	195	9	US-[redacted]	Sequence 7, Applicatio	5.19e-112
20	1240	85.0	195	8	US-[redacted]	Sequence 7, Applicatio	5.19e-112
21	1240	85.0	195	9	US-[redacted]	Sequence 7, Applicatio	5.19e-112
22	1240	85.0	195	10	US-[redacted]	Sequence 7, Applicatio	5.19e-112
23	1240	85.0	195	8	US-[redacted]	Sequence 7, Applicatio	5.19e-112
24	1188	81.5	167	12	US-[redacted]	Sequence 34, Applicati	1.06e-106
25	1162	79.7	160	12	US-[redacted]	Sequence 8, Applicatio	4.75e-104
26	1133	77.7	155	12	US-[redacted]	Sequence 9, Applicatio	4.30e-101
27	1112	76.3	152	12	US-[redacted]	Sequence 10, Applicati	5.94e-99
28	1093	75.0	150	12	US-[redacted]	Sequence 11, Applicati	5.12e-97
29	1073	73.6	147	12	US-[redacted]	Sequence 12, Applicati	5.57e-95
30	1056	72.4	145	12	US-[redacted]	Sequence 13, Applicati	2.99e-93
31	1014	69.5	207	9	US-[redacted]	Sequence 15, Applicati	5.59e-89
32	1014	69.5	207	10	US-[redacted]	Sequence 15, Applicati	5.59e-89
33	1014	69.5	207	9	US-[redacted]	Sequence 15, Applicati	5.59e-89
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36	996	68.3	206	12	US-[redacted]	Sequence 2, Applicatio	3.77e-87
37	946	64.9	221	14	US-[redacted]	Sequence 2, Applicatio	4.49e-82
38	946	64.9	221	12	US-[redacted]	Sequence 5, Applicatio	4.49e-82
39	946	64.9	221	8	US-[redacted]	Sequence 2, Applicatio	4.49e-82
40	946	64.9	221	8	US-[redacted]	Sequence 2, Applicatio	4.49e-82
41	936	64.2	207	9	US-[redacted]	Sequence 13, Applicati	4.64e-81
42	936	64.2	207	9	US-[redacted]	Sequence 13, Applicati	4.64e-81
43	936	64.2	207	9	US-[redacted]	Sequence 13, Applicati	4.64e-81
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ALIGNMENTS

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DE   Sequence 57, Application US/08795430
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CC    Sequence 57, Application US/08795430
CC     GENERAL INFORMATION:
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Joukov, Vladimir
CC       TITLE OF INVENTION:  Vascular Endothelial Growth Factor C (VEGF-C)
CC       TITLE OF INVENTION:  Protein and Gene, Mutants Thereof, and Uses Thereof
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
CC         STREET:  6300 Sears Tower, 233 South Wacker Drive
CC         CITY:  Chicago
CC         STATE:  Illinois
CC         COUNTRY:  United States of America
CC         ZIP:  60606-6402
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/795,430
CC         FILING DATE:
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/FI96/00427
CC         FILING DATE:  01-AUG-1996
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/671,573
CC         FILING DATE:  28-JUN-1996
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/601,132
CC         FILING DATE:  14-FEB-1996
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CC         APPLICATION NUMBER:  08/585,895
CC         FILING DATE:  12-JAN-1996
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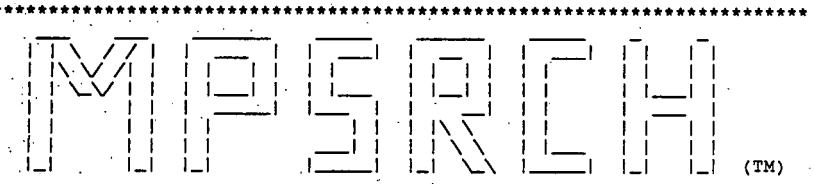


MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:37:39 1998; MasPar time 6.87 Seconds
442.549 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 31.228; Variance 126.442; scale 0.247

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

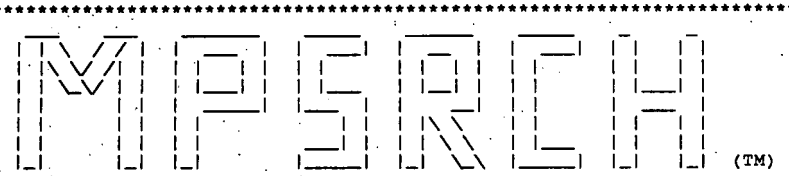
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1458	100.0	188	19	W00726	Vascular endothelial	2.81e-138
2	1458	100.0	188	21	W04829	Fibrosarcoma vascular	2.81e-138
3	1317	90.3	188	21	W04826	Heart vascular endoth	1.89e-123
4	1307	89.6	188	19	W00864	Murine VRF167.	2.12e-122
5	1240	85.0	195	21	W04827	Heart vascular endoth	2.29e-115
6	1023	70.2	143	19	W00727	Vascular endothelial	1.20e-92
7	1014	69.5	207	21	W04831	Vascular endothelial	1.04e-91
8	1014	69.5	207	19	W00725	Vascular endothelial	1.04e-91
9	946	64.9	221	23	W07611	Human vascular endoth	1.29e-84
10	938	64.3	207	21	W04830	Vascular endothelial	8.77e-84
11	928	63.6	207	19	W00863	Murine VRF186.	9.65e-83
12	897	61.5	133	21	W04828	Vascular endothelial	1.63e-79
13	749	51.4	101	19	W00728	Vascular endothelial	3.65e-64
14	709	48.6	102	21	W04824	Vascular endothelial	4.94e-60
15	530	36.4	595	18	W00595	SAP-GlySer-VEGF165(Gl	1.13e-41
16	528	36.2	421	18	W00584	SAP-AlaMet-VEGF165.	1.80e-41
17	528	36.2	588	18	W00592	SAP-AlaMet-VEGF165-Gl	1.80e-41
18	528	36.2	594	18	W00591	SAP-AlaMet-VEGF165(Gl	1.80e-41
19	528	36.2	600	18	W00593	SAP-AlaMet-VEGF165(Gl	1.80e-41
20	521	35.7	192	18	R94040	VEGF165 Cys+2.	9.27e-41
21	521	35.7	428	18	R94072	SAP(Gly4Ser)VEGF165.	9.27e-41
22	521	35.7	443	18	W00585	SAP(Gly4Ser)4VEGF165.	9.27e-41
23	521	35.7	598	18	R94074	SAP(Gly4Ser)VEGF165(G	9.27e-41
24	521	35.7	612	18	W00596	SAP(Gly4Ser)2VEGF165(	9.27e-41
25	517	35.5	165	7	R38921	Human VEGF-165.	2.37e-40
26	518	35.5	191	27	W38242	Vascular endothelial	1.87e-40
27	518	35.5	191	19	W00724	Vascular endothelial	1.87e-40
28	518	35.5	191	18	R94002	VEGF165.	1.87e-40
29	518	35.5	191	2	R08002	Human vascular endoth	1.87e-40
30	518	35.5	191	16	R91076	Human vascular endoth	1.87e-40
31	518	35.5	461	18	W00583	VEGF165-AlaMet-SAP.	1.87e-40
32	517	35.5	595	27	W38235	VEGF/CPG2 fusion prot	2.37e-40
33	517	35.5	607	27	W38237	VEGF/CPG2 fusion prot	2.37e-40
34	513	35.2	190	5	R27350	Sequence of vascular	6.03e-40
35	513	35.2	190	5	R27351	Sequence of vascular	6.03e-40
36	513	35.2	190	4	R22347	Rat Vascular Endothel	6.03e-40
37	513	35.2	190	2	R08120	Mammalian glioma-deri	6.03e-40
38	513	35.2	190	5	R27352	Sequence of vascular	6.03e-40
39	512	35.1	192	18	R94039	VEGF165 Cys+4.	7.62e-40
40	507	34.8	165	25	W31091	Vascular endothelial	2.46e-39
41	506	34.7	165	25	W31086	Vascular endothelial	3.10e-39
42	504	34.6	165	25	W31088	Vascular endothelial	4.95e-39
43	504	34.6	165	25	W31094	Vascular endothelial	4.95e-39
44	505	34.6	190	2	R08001	Bovine vascular endot	3.92e-39
45	503	34.5	165	3	R10917	Human vascular endoth	6.26e-39

ALIGNMENTS

RESULT 1
ID W00726 standard; Protein; 188 AA.
AC W00726;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e6.
KW Vascular endothelial growth factor; VEGF; SOM175-e6; neuron;
KW astroglial proliferation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..21
FT /label= Sig_peptide
PN WO9627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI; 96-412774/41.
DR N-PSDB; T33611.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 12; Page 42-43; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 188 AA;

Query Match 100.0%; Score 1458; DB 19; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.81e-138;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:44:55 1998; MasPar time 2.47 Seconds
537.274 Million cell updates/sec

Tabular output not generated.

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Description: (1-188) from US08765588.pep
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Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CQGRGLELNPDTCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 29.152; Variance 121.909; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1317	90.3	188	1	US-08-469-	Sequence 5, Applicatio	1.60e-120
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6	517	35.5	165	3	5194596-18	Patent No. 5194596.	7.46e-40
7	517	35.5	165	3	5219739-19	Patent No. 5219739.	7.46e-40
8	518	35.5	191	3	5332671-4	Patent No. 5332671.	5.94e-40
9	505	34.6	190	3	5332671-3	Patent No. 5332671.	1.15e-38
10	492	33.7	164	3	5219739-18	Patent No. 5219739.	2.20e-37
11	492	33.7	164	3	5219739-17	Patent No. 5219739.	2.20e-37
12	492	33.7	164	3	5194596-17	Patent No. 5194596.	2.20e-37
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16	383	26.3	121	3	5219739-20	Patent No. 5219739.	1.04e-26
17	377	25.9	231	2	PCT-US96-0	Sequence 10, Applicati	3.99e-26
18	372	25.5	214	3	5240848-11	Patent No. 5240848.	1.22e-25
19	372	25.5	215	3	5219739-22	Patent No. 5219739.	1.22e-25
20	371	25.4	215	3	5240848-7	Patent No. 5240848.	1.53e-25
21	361	24.8	120	3	5219739-9	Patent No. 5219739.	1.42e-24
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24	178	12.2	419	2	PCT-US96-0	Sequence 2, Applicatio	2.27e-07
25	177	12.1	160	1	US-08-094-	Sequence 1, Applicatio	2.79e-07
26	177	12.1	220	3	5175255-4	Patent No. 5175255.	2.79e-07
27	177	12.1	226	3	5498600-2	Patent No. 5498600.	2.79e-07
28	177	12.1	241	3	5175255-2	Patent No. 5175255.	2.79e-07
29	177	12.1	241	3	5175255-8	Patent No. 5175255.	2.79e-07
30	177	12.1	241	3	5194596-15	Patent No. 5194596.	2.79e-07
31	177	12.1	241	1	US-08-387-	Sequence 4, Applicatio	2.79e-07
32	177	12.1	241	3	5219739-15	Patent No. 5219739.	2.79e-07
33	177	12.1	241	1	US-08-469-	Sequence 13, Applicati	2.79e-07
34	177	12.1	241	2	PCT-US96-0	Sequence 9, Applicatio	2.79e-07
35	172	11.8	109	1	US-08-094-	Sequence 3, Applicatio	7.81e-07
36	172	11.8	109	1	US-08-094-	Sequence 5, Applicatio	7.81e-07
37	170	11.7	109	3	5498600-3	Patent No. 5498600.	1.18e-06
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40	170	11.7	109	1	US-08-094-	Sequence 4, Applicatio	1.18e-06
41	170	11.7	109	2	PCT-US91-0	Sequence 18, Applicati	1.18e-06
42	170	11.7	120	3	5428135-2	Patent No. 5428135.	1.18e-06
43	170	11.7	282	1	US-08-445-	Sequence 1, Applicatio	1.18e-06
44	169	11.6	125	1	US-07-883-	Sequence 7, Applicatio	1.45e-06
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ALIGNMENTS

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CC   Patent No. 5607918
CC     GENERAL INFORMATION:
CC       APPLICANT:  Eriksson, Ulf
CC       APPLICANT:  Olofsson, Birgitta
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Pajusola, Katri
CC       TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC       TITLE OF INVENTION:  DNA CODING THEREFOR
CC       NUMBER OF SEQUENCES:  17
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Evenson, McKeown, Edwards & Lenahan
CC         STREET:  1200 G Street, N.W., Suite 700
CC         CITY:  Washington
CC         STATE:  DC
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/469,427A
CC         FILING DATE:  06-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/397,651
CC         FILING DATE:  01-MAR-1995
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Evans, Joseph D
CC         REGISTRATION NUMBER:  26,269
CC         REFERENCE/DOCKET NUMBER:  41979cp2
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (202) 628-8800
CC         TELEFAX:  (202) 628-8844
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  188 amino acids
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MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:34:31 1998; MasPar time 2.64 Seconds
554.454 Million cell updates/sec
Tabular output not generated.

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Description: (1-207) from US08765588.pep
Perfect Score: 1452
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Scoring table: PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 29.438; Variance 149.891; scale 0.196

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1014	69.8	188	1	US-08-469-	Sequence 11, Applicati	3.04e-73
2	938	64.6	188	1	US-08-469-	Sequence 5, Applicatio	6.37e-67
3	897	61.8	133	1	US-08-469-	Sequence 9, Applicatio	1.62e-63
4	861	59.3	195	1	US-08-469-	Sequence 7, Applicatio	1.57e-60
5	709	48.8	102	1	US-08-469-	Sequence 2, Applicatio	5.73e-48
6	379	26.1	214	3	5240848-11	Patent No. 5240848.	4.15e-21
7	379	26.1	231	2	PCT-US96-0	Sequence 10, Applicati	4.15e-21
8	378	26.0	121	3	5219739-20	Patent No. 5219739.	4.99e-21
9	378	26.0	121	3	5194596-19	Patent No. 5194596.	4.99e-21
10	374	25.8	215	3	5219739-22	Patent No. 5219739.	1.04e-20
11	373	25.7	215	3	5240848-7	Patent No. 5240848.	1.25e-20
12	371	25.6	191	3	5332671-4	Patent No. 5332671.	1.80e-20
13	370	25.5	165	3	5219739-19	Patent No. 5219739.	2.17e-20
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15	358	24.7	190	3	5332671-3	Patent No. 5332671.	1.96e-19
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21	344	23.7	189	1	US-08-469-	Sequence 15, Applicati	2.54e-18
22	306	21.1	149	1	US-08-469-	Sequence 14, Applicati	2.55e-15
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24	180	12.4	220	3	5175255-4	Patent No. 5175255.	1.20e-05
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29	180	12.4	241	3	5194596-15	Patent No. 5194596.	1.20e-05
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32	179	12.3	120	3	5428135-2	Patent No. 5428135.	1.42e-05
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34	179	12.3	282	1	US-08-445-	Sequence 1, Applicatio	1.42e-05
35	175	12.1	419	2	PCT-US96-0	Sequence 2, Applicatio	2.80e-05
36	172	11.8	109	1	US-08-094-	Sequence 5, Applicatio	4.66e-05
37	172	11.8	109	1	US-08-094-	Sequence 3, Applicatio	4.66e-05
38	172	11.8	125	2	PCT-US91-0	Sequence 16, Applicati	4.66e-05
39	172	11.8	125	1	US-08-095-	Sequence 4, Applicatio	4.66e-05
40	172	11.8	125	1	US-07-977-	Sequence 7, Applicatio	4.66e-05
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CC    Patent No. 5607918
CC     GENERAL INFORMATION:
CC       APPLICANT:  Eriksson, Ulf
CC       APPLICANT:  Olofsson, Birgitta
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Pajusola, Katri
CC       TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC       TITLE OF INVENTION:  DNA CODING THEREFOR
CC       NUMBER OF SEQUENCES:  17
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Evenson, McKeown, Edwards & Lenahan
CC         STREET:  1200 G Street, N.W., Suite 700
CC         CITY:  Washington
CC         STATE:  DC
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/469,427A
CC         FILING DATE:  06-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/397,651
CC         FILING DATE:  01-MAR-1995
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Evans, Joseph D
CC         REGISTRATION NUMBER:  26,269
CC         REFERENCE/DOCKET NUMBER:  41979cp2
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (202) 628-8800
CC         TELEFAX:  (202) 628-8844
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  188 amino acids
```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:34:57 1998; MasPar time 11.31 Seconds
579.235 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....PGPAAAAADAAASSVAKGGA 207

Scoring table: PAM 150
Gap 11

Searched: 288199 seqs, 31643258 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP
17:NEWU6 18:NEWU7 19:NEWU8 20:NEWU9

Statistics: Mean 31.271; Variance 155.127; scale 0.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1452	100.0	207	10	US-	Sequence 15, Applicati	1.32e-111
2	1452	100.0	207	9	US-	Sequence 15, Applicati	1.32e-111
3	1452	100.0	207	9	US-	Sequence 15, Applicati	1.32e-111
4	1452	100.0	207	9	US-	Sequence 15, Applicati	1.32e-111
5	1452	100.0	207	10	US-	Sequence 15, Applicati	1.32e-111
6	1434	98.8	206	12	US-	Sequence 2, Applicatio	4.66e-110
7	1317	90.7	207	9	US-	Sequence 13, Applicati	5.20e-100
8	1317	90.7	207	9	US-	Sequence 13, Applicati	5.20e-100
9	1317	90.7	207	9	US-	Sequence 13, Applicati	5.20e-100
10	1317	90.7	207	10	US-	Sequence 13, Applicati	5.20e-100
11	1317	90.7	207	10	US-	Sequence 13, Applicati	5.20e-100
12	1287	88.6	185	12	US-	Sequence 35, Applicati	1.95e-97
13	1243	85.6	178	12	US-	Sequence 14, Applicati	1.15e-93
14	1203	82.9	173	12	US-	Sequence 15, Applicati	3.08e-90
15	1160	79.9	168	12	US-	Sequence 16, Applicati	1.48e-86
16	1123	77.3	163	12	US-	Sequence 17, Applicati	2.16e-83
17	1114	76.7	221	14	US-	Sequence 2, Applicatio	1.27e-82
18	1114	76.7	221	8	US-	Sequence 2, Applicatio	1.27e-82
19	1114	76.7	221	8	US-	Sequence 2, Applicatio	1.27e-82
20	1106	76.2	221	12	US-	Sequence 5, Applicatio	6.14e-82
21	1083	74.6	201	12	US-	Sequence 36, Applicati	5.67e-80
22	1039	71.6	194	12	US-	Sequence 18, Applicati	3.24e-76
23	1014	69.8	188	9	US-	Sequence 11, Applicati	4.40e-74
24	1014	69.8	188	10	US-	Sequence 11, Applicati	4.40e-74
25	1014	69.8	188	10	US-	Sequence 11, Applicati	4.40e-74
26	1014	69.8	188	11	US-	Sequence 57, Applicati	4.40e-74
27	1014	69.8	188	9	US-	Sequence 11, Applicati	4.40e-74
28	1014	69.8	188	10	US-	Sequence 56, Applicati	4.40e-74
29	1014	69.8	188	9	US-	Sequence 11, Applicati	4.40e-74
30	1014	69.8	188	8	US-	Sequence 11, Applicati	4.40e-74
31	999	68.8	189	12	US-	Sequence 19, Applicati	8.36e-73
32	956	65.8	184	12	US-	Sequence 20, Applicati	3.86e-69
33	941	64.8	188	12	US-	Sequence 1, Applicatio	7.30e-68
34	938	64.6	188	9	US-	Sequence 5, Applicatio	1.31e-67
35	938	64.6	188	8	US-	Sequence 5, Applicatio	1.31e-67
36	938	64.6	188	9	US-	Sequence 5, Applicatio	1.31e-67
37	938	64.6	188	9	US-	Sequence 5, Applicatio	1.31e-67
38	938	64.6	188	8	US-	Sequence 5, Applicatio	1.31e-67
39	938	64.6	188	10	US-	Sequence 5, Applicatio	1.31e-67
40	938	64.6	188	10	US-	Sequence 5, Applicatio	1.31e-67
41	919	63.3	179	12	US-	Sequence 21, Applicati	5.43e-66
42	897	61.8	133	10	US-	Sequence 9, Applicatio	4.03e-64
43	897	61.8	133	8	US-	Sequence 9, Applicatio	4.03e-64
44	897	61.8	133	8	US-	Sequence 9, Applicatio	4.03e-64
45	897	61.8	133	9	US-	Sequence 9, Applicatio	4.03e-64

ALIGNMENTS

RESULT 1
ID US-08-609-443A-15 STANDARD; PRT; 207 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 15, Application US/08609443A
XX
CC Sequence 15, Application US/08609443A
CC GENERAL INFORMATION:
CC APPLICANT: ERIKSSON, Ulf
CC APPLICANT: OLOFSSON, Birgitta
CC APPLICANT: ALITALO, Kari
CC APPLICANT: PAJUSOLA, Katri
CC TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC TITLE OF INVENTION: DNA CODING THEREFOR
CC NUMBER OF SEQUENCES: 31
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
CC STREET: 1200 G Street, N.W., Suite 700
CC CITY: Washington
CC STATE: DC
CC COUNTRY: US
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/609,443A
CC FILING DATE: 01-MAR-1996
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/397,651
CC FILING DATE: 01-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/469,427
CC FILING DATE: 06-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/569,063
CC FILING DATE: 06-DEC-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: EVANS, Joseph D
CC REGISTRATION NUMBER: 26,269

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:32:46 1998; MasPar time 11.91 Seconds
732.057 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....PGPAAAAADAAASSVAKGGA 207

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 42.614; Variance 109.241; scale 0.390

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

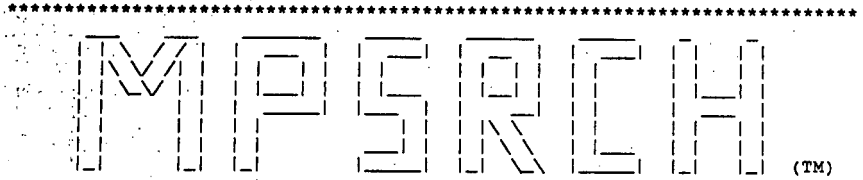
Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1452	100.0	207	2	Q16528	VEGF RELATED FACTOR IS	2.09e-211
2	1319	90.8	207	10	Q64290	VASCULAR ENDOTHELIAL G	1.59e-189
3	780	53.7	116	10	O35485	VASCULAR ENDOTHELIAL G	9.13e-102
4	373	25.7	232	2	Q16889	VASCULAR ENDOTHELIAL G	8.56e-38
5	372	25.6	148	12	O42571	VASCULAR ENDOTHELIAL G	1.21e-37
6	361	24.9	194	12	O42572	VASCULAR ENDOTHELIAL G	5.56e-36
7	333	22.9	216	12	Q91420	VASCULAR ENDOTHELIAL G	8.83e-32
8	279	19.2	158	10	Q63434	PLACENTA GROWTH FACTOR	8.04e-24
9	278	19.1	75	4	O18843	VASCULAR ENDOTHELIAL G	1.12e-23
10	198	13.6	358	10	P97946	VASCULAR ENDOTHELIAL G	2.14e-12
11	196	13.5	210	4	Q29613	C-SIS ONCOGENE (PLATEL	4.00e-12
12	192	13.2	326	10	O35251	VASCULAR ENDOTHELIAL G	1.39e-11
13	180	12.4	271	11	O41283	POLYPROTEIN PRECURSOR	5.55e-10
14	179	12.3	185	2	Q15354	C-SIS PROTO-ONCOGENE (	7.52e-10
15	176	12.1	415	10	P97953	VASCULAR ENDOTHELIAL G	1.87e-09
16	162	11.2	183	10	Q63740	PDGF PROTEIN (FRAGMENT	1.24e-07
17	153	10.5	473	8	Q39620	(VSP-3) PRECURSOR.	1.73e-06
18	143	9.8	581	3	Q20517	F47B8.5.	3.04e-05
19	141	9.7	901	9	Q44562	SIALIDASE.	5.35e-05
20	139	9.6	442	8	Q39494	75K MRNA.	9.38e-05
21	137	9.4	2378	3	P91365	CODED FOR BY C. ELEGAN	1.64e-04
22	134	9.2	552	8	Q96343	MYROSINASE-BINDING PRO	3.78e-04
23	132	9.1	438	8	Q39495	ALPHA 2 FRUSTULIN.	6.55e-04
24	130	9.0	371	9	O06555	HYPOTHETICAL 36.4 KD P	1.13e-03
25	130	9.0	416	3	O17374	T13B5.4 PROTEIN.	1.13e-03
26	130	9.0	611	9	P74375	HYPOTHETICAL 62.9 KD P	1.13e-03
27	131	9.0	1356	10	Q63729	N-METHYL-D-ASPARTATE R	8.62e-04
28	129	8.9	351	8	Q39492	WP6 PRECURSOR.	1.49e-03
29	129	8.9	375	8	P93066	OLEOSIN-LIKE PROTEIN.	1.49e-03
30	129	8.9	376	8	Q39353	CELL WALL-PLASMA MEMBR	1.49e-03
31	129	8.9	381	3	Q94399	ZK265.2.	1.49e-03
32	129	8.9	507	12	O13028	ANTIFREEZE GLYCOPEPTID	1.49e-03
33	128	8.8	151	8	Q41192	NAPRP3.	1.95e-03
34	128	8.8	196	8	Q08195	CYSTEINE-RICH EXTENSIN	1.95e-03
35	128	8.8	439	8	Q42421	CHITINASE PRECURSOR.	1.95e-03
36	128	8.8	1711	9	P96311	ENDOGLUCANASE A (EC 3.	1.95e-03
37	127	8.7	145	8	Q40786	ARABINOGALACTAN-PROTEI	2.56e-03
38	127	8.7	153	3	O00879	MEROZOITE SURFACE PROT	2.56e-03
39	127	8.7	309	11	Q89402	CONTAINS PRO-RICH PX M	2.56e-03
40	127	8.7	464	8	Q41645	EXTENSIN (FRAGMENT).	2.56e-03
41	127	8.7	801	3	Q23635	SIMILAR TO LONG TANDEM	2.56e-03
42	125	8.6	228	8	Q43558	PROLINE RICH PROTEIN P	4.39e-03
43	125	8.6	616	11	Q96716	DNA BINDING PROTEIN.	4.39e-03
44	124	8.5	496	11	Q98457	GENOME, PARTIAL SEQUEN	5.74e-03
45	124	8.5	1000	9	O24820	BETA-GLUCANASE.	5.74e-03

ALIGNMENTS

RESULT 1
ID Q16528 PRELIMINARY; PRT; 207 AA.
AC Q16528;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.
GN VRF OR VEGF-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
RA HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96325041.
RA OLOFSSON B., PAJUSOLA K., VON EULER G., CHILOV D., ALITALO K.,
RA ERIKSSON U.;
RL J. BIOL. CHEM. 271:19310-19317(1996).
DR EMBL; U43368; G1216396; -.
DR EMBL; U52819; G1488259; -.
DR PROSITE; PS00249; PDGF; 1.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 207 VEGF RELATED FACTOR ISOFORM VRF186.
SQ SEQUENCE 207 AA; 21602 MW; 16BDF6F1 CRC32;

Query Match 100.0%; Score 1452; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.09e-211;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:31:58 1998; MasPar time 6.68 Seconds
777.434 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....PGPAAAAADAAASSVAKGGA 207

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 44.541; Variance 104.798; scale 0.425

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

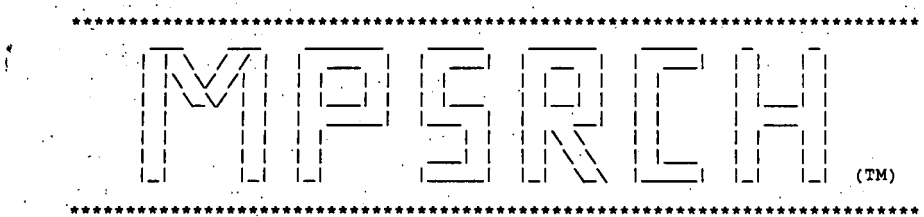
Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1014	69.8	188	1	VEGB_HUMAN	VASCULAR ENDOTHELIAL G	1.62e-151
2	938	64.6	188	1	VEGB_MOUSE	VASCULAR ENDOTHELIAL G	4.30e-138
3	373	25.7	215	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	5.93e-41
4	371	25.6	190	1	VEGF_RAT	VASCULAR ENDOTHELIAL G	1.26e-40
5	371	25.6	214	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	1.26e-40
6	364	25.1	190	1	VEGF_PIG	VASCULAR ENDOTHELIAL G	1.76e-39
7	361	24.9	146	1	VEGF_SHEEP	VASCULAR ENDOTHELIAL G	5.43e-39
8	358	24.7	190	1	VEGF_BOVIN	VASCULAR ENDOTHELIAL G	1.68e-38
9	347	23.9	164	1	VEGF_CAVPO	VASCULAR ENDOTHELIAL G	1.03e-36
10	306	21.1	170	1	PLGF_HUMAN	PLACENTA GROWTH FACTOR	4.08e-30
11	294	20.2	133	1	VEGH_ORFN2	VASCULAR ENDOTHELIAL G	3.29e-28
12	284	19.6	158	1	PLGF_MOUSE	PLACENTA GROWTH FACTOR	1.25e-26
13	264	18.2	128	1	VEGF_COTJA	VASCULAR ENDOTHELIAL G	1.68e-23
14	189	13.0	225	1	PDGB_RAT	PLATELET-DERIVED GROWT	3.15e-12
15	180	12.4	226	1	TSIS_SMSAV	PDGF-RELATED TRANSFORM	6.10e-11
16	180	12.4	241	1	PDGB_HUMAN	PLATELET-DERIVED GROWT	6.10e-11
17	179	12.3	241	1	PDGB_MOUSE	PLATELET-DERIVED GROWT	8.46e-11
18	179	12.3	245	1	PDGB_FELCA	PLATELET-DERIVED GROWT	8.46e-11
19	175	12.1	419	1	VEGC_HUMAN	VASCULAR ENDOTHELIAL G	3.11e-10
20	174	12.0	148	1	VEGH_ORFN7	VASCULAR ENDOTHELIAL G	4.30e-10
21	172	11.8	211	1	PDGA_HUMAN	PLATELET-DERIVED GROWT	8.21e-10
22	172	11.8	213	1	PDGA_RABIT	PLATELET-DERIVED GROWT	8.21e-10
23	167	11.5	211	1	PDGA_MOUSE	PLATELET-DERIVED GROWT	4.09e-09
24	165	11.4	204	1	PDGA_RAT	PLATELET-DERIVED GROWT	7.73e-09
25	163	11.2	226	1	PDGA_XENLA	PLATELET-DERIVED GROWT	1.46e-08
26	162	11.2	241	1	PDGB_SHEEP	PLATELET-DERIVED GROWT	2.00e-08
27	144	9.9	279	1	Y091_NPVOP	HYPOTHETICAL 29.3 KD P	5.32e-06
28	136	9.4	439	1	XP2_XENLA	SKIN SECRETORY PROTEIN	5.85e-05
29	137	9.4	474	1	VTP3_TTV1V	VIRAL PROTEIN TPX.	4.35e-05
30	136	9.4	699	1	VGLG_HSV2H	GLYCOPROTEIN G.	5.85e-05
31	134	9.2	775	1	ICP0_HSV11	TRANS-ACTING TRANSCRIP	1.06e-04
32	128	8.8	3149	1	TEGU_EBV	LARGE TEGUMENT PROTEIN	6.07e-04
33	126	8.7	316	1	CDNC_HUMAN	CYCLIN-DEPENDENT KINAS	1.08e-03
34	126	8.7	409	1	R23B_HUMAN	UV EXCISION REPAIR PRO	1.08e-03
35	126	8.7	485	1	SSGP_VOLCA	SULFATED SURFACE GLYCO	1.08e-03
36	126	8.7	534	1	APG_ARATH	ANTER-SPECIFIC PROLINE	1.08e-03
37	126	8.7	5179	1	MUC2_HUMAN	MUCIN 2 PRECURSOR (INT	1.08e-03
38	123	8.5	308	1	CC40_CAEEL	CUTICLE COLLAGEN 40.	2.54e-03
39	123	8.5	1446	1	IE18_PRVKA	IMMEDIATE-EARLY PROTEI	2.54e-03
40	122	8.4	344	1	ME18_HUMAN	DNA-BINDING PROTEIN ME	3.36e-03
41	122	8.4	1461	1	IE18_PRVIF	IMMEDIATE-EARLY PROTEI	3.36e-03
42	120	8.3	449	1	APG_BRANA	ANTER-SPECIFIC PROLINE	5.90e-03
43	120	8.3	1323	1	NME4_MOUSE	GLUTAMATE (NMDA) RECEP	5.90e-03
44	119	8.2	380	1	VASP_HUMAN	VASODILATOR-STIMULATED	7.80e-03
45	119	8.2	600	1	SP96_DICDI	SPORE COAT PROTEIN SP9	7.80e-03

ALIGNMENTS

```
RESULT    1
ID   VEGB_HUMAN     STANDARD;      PRT;   188 AA.
AC   P49765;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE   FACTOR).
GN   VEGFB OR VRF.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96197355.
RA   OLOFSSON B., PAJUSOLA K., KAIPAINEN A., VON EULER G., JOUKOV V.,
RA   SAKSELA O., ORPANA A., PETTERSSON R.F., ALITALO K., ERIKSSON U.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA   POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,
RA   WARD L., HAYWARD N., WEBER G.;
RL   GENOME RES. 6:122-129(1996).
CC   -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC       WITH VEGF.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC       HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR   EMBL; U48801; G1234823; -.
DR   EMBL; U43369; G1216398; -.
DR   MIM; 601398; -.
DR   PROSITE; PS00249; PDGF; 1.
KW   MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    188       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   188 AA;  21261 MW;  35EA8904 CRC32;

  Query Match          69.8%;  Score 1014;  DB 1;  Length 188;
  Best Local Similarity 100.0%;  Pred. No. 1.62e-151;
  Matches   136;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:30:29 1998; MasPar time 9.90 Seconds
763.780 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....PGPAAAAADAAASSVAKGGA 207

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 42.396; Variance 117.569; scale 0.361

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1319	90.8	207	2	JC4679	vascular endothelial	3.19e-175
2	938	64.6	188	2	JC4680	vascular endothelial	1.15e-117
3	373	25.7	232	2	A41551	vascular endothelial	7.14e-35
4	371	25.6	190	2	A35987	glioma-derived vascul	1.36e-34
5	371	25.6	214	2	A44881	vascular endothelial	1.36e-34
6	367	25.3	190	2	B44881	vascular endothelial	4.94e-34
7	364	25.1	190	2	S52130	vascular endothelial	1.30e-33
8	361	24.9	146	2	S57956	ovine vascular endoth	3.40e-33
9	358	24.7	190	2	B40080	vascular endothelial	8.91e-33
10	353	24.3	120	2	A33787	vascular endothelial	4.43e-32
11	306	21.1	149	2	A41236	placental growth fact	1.35e-25
12	293	20.2	133	2	B49530	vascular endothelial	7.91e-24
13	279	19.2	158	2	A56125	placental growth fact	6.17e-22
14	264	18.2	128	2	I51295	vascular endothelial	6.32e-20
15	189	13.0	225	2	S25097	platelet-derived grow	3.18e-10
16	180	12.4	161	2	I38108	platelet-derived grow	4.12e-09
17	180	12.4	226	1	TVMVSS	PDGF-related transfor	4.12e-09
18	180	12.4	230	2	A55030	platelet-derived grow	4.12e-09
19	180	12.4	241	1	PFHUG2	platelet-derived grow	4.12e-09
20	179	12.3	185	2	S58383	hypothetical protein	5.47e-09
21	179	12.3	241	1	PFMSGB	platelet-derived grow	5.47e-09
22	179	12.3	245	1	TVCTSS	platelet-derived grow	5.47e-09
23	175	12.1	166	2	JN0248	platelet-derived grow	1.69e-08
24	175	12.1	419	2	S69207	vascular endothelial	1.69e-08
25	174	12.0	148	2	D49530	16K vascular endothel	2.23e-08
26	171	11.8	198	2	JS0735	platelet-derived grow	5.16e-08
27	172	11.8	211	1	PFHUG1	platelet-derived grow	3.90e-08
28	165	11.4	197	2	S25096	platelet-derived grow	2.72e-07
29	166	11.4	271	2	A25669	PDGF-related transfor	2.07e-07
30	164	11.3	196	2	B28964	platelet-derived grow	3.59e-07
31	163	11.2	200	2	I51551	platelet-derived grow	4.72e-07
32	163	11.2	215	2	S08220	platelet-derived grow	4.72e-07
33	163	11.2	226	2	I51550	platelet-derived grow	4.72e-07
34	161	11.1	196	2	A37359	platelet-derived grow	8.17e-07
35	153	10.5	63	5	1PDGB2	Platelet-derived grow	7.18e-06
36	153	10.5	66	5	1PDGC2	Platelet-derived grow	7.18e-06
37	153	10.5	68	5	1PDGA2	Platelet-derived grow	7.18e-06
38	153	10.5	473	2	S50755	hypothetical protein	7.18e-06
39	145	10.0	196	2	A48851	platelet-derived grow	6.08e-05
40	141	9.7	901	2	A49227	sialidase - Actinomyc	1.74e-04
41	139	9.6	442	2	S50062	cell wall glycoprotei	2.94e-04
42	136	9.4	416	1	SKXLAG	dermal gland protein	6.39e-04
43	137	9.4	474	2	S15921	protein TPX-VT3 - The	4.94e-04
44	136	9.4	699	2	C43674	US4 protein - human h	6.39e-04
45	135	9.3	377	2	A48018	mucin 7 precursor, sa	8.27e-04

ALIGNMENTS

```
RESULT    1
ENTRY             JC4679     #type complete
TITLE             vascular endothelial growth factor-related factor 186 - mouse
ALTERNATE_NAMES   VRF 186 protein, VEGF 186
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              10-May-1996 #sequence_revision 19-Jul-1996 #text_change
                    10-Sep-1997
ACCESSIONS        JC4679
REFERENCE         JC4679
   #authors       Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
                    Nordenskjoeld, M.; Weber, G.; Hayward, N.
   #journal       Biochem. Biophys. Res. Commun. (1996) 220:922-928
   #title         Characterization of the murine VEGF-related factor gene.
   #accession     JC4679
      ##molecule_type mRNA
      ##residues      1-207 ##label TOW
      ##cross-references GB:U43836; NID:g1703480; PID:g1314334
COMMENT     This factor is a mitogen, that is selective for endothelial cells,
              and belongs to a family of growth factors. This transcript is
              differentially spliced to produce two major isoforms, vascular
              endothelial growth factors 167 and 186.
GENETICS
   #gene          vrf
   #map_position 19
KEYWORDS          growth factor
FEATURE
   1-21                #domain signal sequence #status predicted #label SIG\
   22-207              #product vascular endothelial growth factor related
                         factor #status predicted #label MAT
SUMMARY           #length 207  #molecular-weight 21914  #checksum 1525

  Query Match           90.8%;  Score 1319;  DB 2;  Length 207;
  Best Local Similarity  87.0%;  Pred. No. 3.19e-175;
  Matches   180;  Conservative   17;  Mismatches  10;  Indels   0;  Gaps   0;

Db       1 MSPLLRRLLLVALLQLARTQAPVSQFDGPSHQKKVVPWIDVYARATCQPREVVVPLSMEL 60
           |||||||||| |||||| :|||||| |:|:||:|||:|||||:|||||||||||||::||
Qy       1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

Db      61 MGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIQYPSSQLGEMSLEEHS 120
           || | ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Qy      61 MGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIRYPSSQLGEMSLEEHS 120

Db     121 QCECRPKKKESAVKPDRVAIPHHRPQPRSVPGWDSTPGASSPADIIHPTPAPGSSARLAP 180
           |||||||||:||||||| | ||||||||||||||:|||:||||| |||||||:|| ||
Qy     121 QCECRPKKKDSAVKPDRAATPHHRPQPRSVPGWDSAPGAPSPADITHPTPAPGPSAHAAP 180
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:28:23 1998; MasPar time 7.27 Seconds
460.975 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....PGPAAAAADAAASSVAKGGA 207

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 31.715; Variance 158.417; scale 0.200

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1452	100.0	207	19	W00725	Vascular endothelial	5.23e-111
2	1452	100.0	207	21	W04831	Vascular endothelial	5.23e-111
3	1319	90.8	207	21	W04830	Vascular endothelial	1.15e-99
4	1310	90.2	207	19	W00863	Murine VRF186.	6.70e-99
5	1114	76.7	221	23	W07611	Human vascular endoth	3.11e-82
6	1023	70.5	143	19	W00727	Vascular endothelial	1.61e-74
7	1014	69.8	188	19	W00726	Vascular endothelial	9.33e-74
8	1014	69.8	188	21	W04829	Fibrosarcoma vascular	9.33e-74
9	938	64.6	188	21	W04826	Heart vascular endoth	2.50e-67
10	928	63.9	188	19	W00864	Murine VRF167.	1.75e-66
11	897	61.8	133	21	W04828	Vascular endothelial	7.23e-64
12	861	59.3	195	21	W04827	Heart vascular endoth	7.84e-61
13	749	51.6	101	19	W00728	Vascular endothelial	2.05e-51
14	709	48.8	102	21	W04824	Vascular endothelial	4.59e-48
15	395	27.2	500	18	W00589	SAP-AlaMet-VEGF121-Gl	4.14e-22
16	389	26.8	377	18	W00586	SAP-AlaMet-VEGF121.	1.27e-21
17	389	26.8	506	18	W00588	SAP-AlaMet-VEGF121(Gl	1.27e-21
18	389	26.8	512	18	W00590	SAP-AlaMet-VEGF121(Gl	1.27e-21
19	383	26.4	146	5	R27354	Sequence of vascular	3.89e-21
20	383	26.4	146	4	R22348	Alternative form of V	3.89e-21
21	383	26.4	595	18	W00595	SAP-GlySer-VEGF165(Gl	3.89e-21
22	382	26.3	148	18	R94032	VEGF121 Cys+2.	4.69e-21
23	382	26.3	384	18	R94071	SAP(Gly4Ser)VEGF121.	4.69e-21
24	382	26.3	399	18	W00587	SAP(Gly4Ser)4VEGF121.	4.69e-21
25	382	26.3	514	18	R94073	SAP(Gly4Ser)VEGF121(G	4.69e-21
26	382	26.3	524	18	W00594	SAP(Gly4Ser)2VEGF121(	4.69e-21
27	381	26.2	421	18	W00584	SAP-AlaMet-VEGF165.	5.65e-21
28	381	26.2	588	18	W00592	SAP-AlaMet-VEGF165-Gl	5.65e-21
29	381	26.2	594	18	W00591	SAP-AlaMet-VEGF165(Gl	5.65e-21
30	381	26.2	600	18	W00593	SAP-AlaMet-VEGF165(Gl	5.65e-21
31	379	26.1	147	16	R91075	Human vascular endoth	8.20e-21
32	379	26.1	147	18	R94001	VEGF121.	8.20e-21
33	378	26.0	121	3	R11385	Human vascular endoth	9.88e-21
34	378	26.0	121	7	R42607	Human VEGF-121.	9.88e-21
35	377	26.0	546	27	W38234	VEGF/CPG2 fusion prot	1.19e-20
36	374	25.8	192	18	R94040	VEGF165 Cys+2.	2.08e-20
37	375	25.8	214	4	R22351	Alternative form of V	1.73e-20
38	375	25.8	214	5	R27355	Sequence of vascular	1.73e-20
39	374	25.8	428	18	R94072	SAP(Gly4Ser)VEGF165.	2.08e-20
40	374	25.8	443	18	W00585	SAP(Gly4Ser)4VEGF165.	2.08e-20
41	374	25.8	598	18	R94074	SAP(Gly4Ser)VEGF165(G	2.08e-20
42	374	25.8	612	18	W00596	SAP(Gly4Ser)2VEGF165(	2.08e-20
43	373	25.7	215	16	R91077	Human vascular endoth	2.51e-20
44	373	25.7	215	1	R05102	Human vascular permea	2.51e-20
45	373	25.7	232	18	R94004	VEGF206.	2.51e-20

ALIGNMENTS

RESULT 1
ID W00725 standard; Protein; 207 AA.
AC W00725;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175.
KW Vascular endothelial growth factor; VEGF; VEGF165; SOM175; neuron;
KW astroglial proliferation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..21
FT /label= Sig_peptide
PN WO9627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI; 96-412774/41.
DR N-PSDB; T33610.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 11; Page 41; 113pp; English.
CC Human vascular endothelial growth factor (VEGF)-like polypeptide
CC (W00725) is capable inducing the proliferation of vascular
CC endothelial cells, of interacting with flt-1/fkl-1 receptors,
CC and of inducing cell migration, cell survival and/or an increase
CC in intracellular levels of alkaline phosphatase. It shows 33.3%
CC identity with human VEGF (see also W00724). Splice variants
CC (W00726-28) of SOM175 have also been identified. Recombinant SOM175
CC can be produced in host cells transformed with vectors carrying
CC SOM175 cDNA (see also T33610). It is useful for inducing astroglial
CC proliferation and for promoting neural survival and/or proliferation.
SQ Sequence 207 AA;

Query Match 100.0%; Score 1452; DB 19; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.23e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:58:22 1998; MasPar time 7.36 Seconds
577.863 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 38.781; Variance 69.409; scale 0.559

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	749	99.3	207	2	Q16528	VEGF RELATED FACTOR IS	2.19e-142
2	682	90.5	207	10	Q64290	VASCULAR ENDOTHELIAL G	5.75e-127
3	361	47.9	116	10	O35485	VASCULAR ENDOTHELIAL G	9.20e-55
4	256	34.0	232	2	Q16889	VASCULAR ENDOTHELIAL G	2.39e-32
5	240	31.8	148	12	O42571	VASCULAR ENDOTHELIAL G	4.85e-29
6	240	31.8	194	12	O42572	VASCULAR ENDOTHELIAL G	4.85e-29
7	229	30.4	216	12	Q91420	VASCULAR ENDOTHELIAL G	8.66e-27
8	206	27.3	158	10	Q63434	PLACENTA GROWTH FACTOR	3.78e-22
9	170	22.5	75	4	O18843	VASCULAR ENDOTHELIAL G	4.06e-15
10	170	22.5	358	10	P97946	VASCULAR ENDOTHELIAL G	4.06e-15
11	170	22.5	415	10	P97953	VASCULAR ENDOTHELIAL G	4.06e-15
12	164	21.8	326	10	O35251	VASCULAR ENDOTHELIAL G	5.58e-14
13	153	20.3	210	4	Q29613	C-SIS ONCOGENE (PLATEL	6.33e-12
14	150	19.9	185	2	Q15354	C-SIS PROTO-ONCOGENE (	2.26e-11
15	150	19.9	271	11	O41283	POLYPROTEIN PRECURSOR	2.26e-11
16	129	17.1	183	10	Q63740	PDGF PROTEIN (FRAGMENT	1.31e-07
17	112	14.9	126	10	O35757	VASCULAR ENDOTHELIAL G	1.00e-04
18	93	12.3	411	8	Q38946	GLUTAMATE DEHYDROGENAS	9.68e-02
19	89	11.8	571	9	Q51763	IS1162 DNA.	3.75e-01
20	87	11.5	411	8	O04937	NADH GLUTAMATE DEHYDRO	7.27e-01
21	86	11.4	394	9	P96447	EXPA6.	1.01e+00
22	86	11.4	605	2	O00304	VOLTAGE-DEPENDENT CALC	1.01e+00
23	85	11.3	411	8	O04872	GLUTAMATE DEHYDROGENAS	1.40e+00
24	85	11.3	411	8	Q43260	GLUTAMATE DEHYDROGENAS	1.40e+00
25	85	11.3	411	8	O04871	GLUTAMATE DEHYDROGENAS	1.40e+00
26	85	11.3	412	8	P93541	GLUTAMATE DEHYDROGENAS	1.40e+00
27	85	11.3	423	10	P97569	KALLISTATIN.	1.40e+00
28	84	11.1	641	10	Q08463	FRIZZLED PROTEIN HOMOL	1.93e+00
29	83	11.0	393	9	Q46413	(INDIVIDUAL ISOLATE 11	2.65e+00
30	83	11.0	393	9	Q46410	MAJOR OUTER MEMBRANE P	2.65e+00
31	83	11.0	393	9	Q46412	MAJOR OUTER MEMBRANE P	2.65e+00
32	83	11.0	393	9	Q46414	MAJOR OUTER MEMBRANE P	2.65e+00
33	83	11.0	393	9	Q46411	(INDIVIDUAL ISOLATE 98	2.65e+00
34	83	11.0	393	9	Q46415	MAJOR OUTER MEMBRANE P	2.65e+00
35	83	11.0	393	9	Q46409	MAJOR OUTER MEMBRANE P	2.65e+00
36	83	11.0	394	9	O06020	MAJOR OUTER MEMBRANE P	2.65e+00
37	83	11.0	394	9	Q46408	MAJOR OUTER MEMBRANE P	2.65e+00
38	83	11.0	396	9	Q46406	MAJOR OUTER MEMBRANE P	2.65e+00
39	83	11.0	722	3	Q19738	F22E12.1 (FRAGMENT).	2.65e+00
40	83	11.0	1031	3	O09489	ORGANELLE-TYPE CALCIUM	2.65e+00
41	83	11.0	4096	2	Q13327	DNA DEPENDENT PROTEIN	2.65e+00
42	83	11.0	4127	2	P78527	DNA-DEPENDENT PROTEIN	2.65e+00
43	82	10.9	488	11	Q03822	ENV POLYPROTEIN (CONTA	3.64e+00
44	82	10.9	619	10	Q62309	TESTIS NUCLEAR RNA-BIN	3.64e+00
45	82	10.9	684	2	Q14050	ALPHA-3 TYPE IX COLLAG	3.64e+00

ALIGNMENTS

RESULT 1
ID Q16528 PRELIMINARY; PRT; 207 AA.
AC Q16528;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.
GN VRF OR VEGF-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
RA HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROSARCOMA HT-1080;
RX MEDLINE; 96325041.
RA OLOFSSON B., PAJUSOLA K., VON EULER G., CHILOV D., ALITALO K.,
RA ERIKSSON U.;
RL J. BIOL. CHEM. 271:19310-19317(1996).
DR EMBL; U43368; G1216396; -.
DR EMBL; U52819; G1488259; -.
DR PROSITE; PS00249; PDGF; 1.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 207 VEGF RELATED FACTOR ISOFORM VRF186.
SQ SEQUENCE 207 AA; 21602 MW; 16BDF6F1 CRC32;

Query Match 99.3%; Score 749; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.19e-142;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:57:41 1998; MasPar time 4.15 Seconds
610.764 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 40.632; Variance 65.664; scale 0.619

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	749	99.3	188	1	VEGB_HUMAN	VASCULAR ENDOTHELIAL G	9.02e-157
2	682	90.5	188	1	VEGB_MOUSE	VASCULAR ENDOTHELIAL G	9.55e-140
3	256	34.0	215	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	1.71e-35
4	249	33.0	190	1	VEGF_PIG	VASCULAR ENDOTHELIAL G	6.68e-34
5	244	32.4	190	1	VEGF_RAT	VASCULAR ENDOTHELIAL G	9.07e-33
6	240	31.8	190	1	VEGF_BOVIN	VASCULAR ENDOTHELIAL G	7.25e-32
7	240	31.8	214	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	7.25e-32
8	235	31.2	146	1	VEGF_SHEEP	VASCULAR ENDOTHELIAL G	9.66e-31
9	232	30.8	133	1	VEGH_ORFN2	VASCULAR ENDOTHELIAL G	4.55e-30
10	229	30.4	164	1	VEGF_CAVPO	VASCULAR ENDOTHELIAL G	2.13e-29
11	218	28.9	170	1	PLGF_HUMAN	PLACENTA GROWTH FACTOR	5.93e-27
12	209	27.7	158	1	PLGF_MOUSE	PLACENTA GROWTH FACTOR	5.67e-25
13	172	22.8	148	1	VEGH_ORFN7	VASCULAR ENDOTHELIAL G	4.73e-17
14	166	22.0	419	1	VEGC_HUMAN	VASCULAR ENDOTHELIAL G	8.31e-16
15	160	21.2	128	1	VEGF_COTJA	VASCULAR ENDOTHELIAL G	1.42e-14
16	157	20.8	225	1	PDGB_RAT	PLATELET-DERIVED GROWT	5.77e-14
17	153	20.3	245	1	PDGB_FELCA	PLATELET-DERIVED GROWT	3.71e-13
18	152	20.2	241	1	PDGB_MOUSE	PLATELET-DERIVED GROWT	5.89e-13
19	150	19.9	226	1	TSIS_SMSAV	PDGF-RELATED TRANSFORM	1.48e-12
20	150	19.9	241	1	PDGB_HUMAN	PLATELET-DERIVED GROWT	1.48e-12
21	149	19.8	241	1	PDGB_SHEEP	PLATELET-DERIVED GROWT	2.35e-12
22	138	18.3	213	1	PDGA_RABIT	PLATELET-DERIVED GROWT	3.42e-10
23	132	17.5	211	1	PDGA_MOUSE	PLATELET-DERIVED GROWT	4.88e-09
24	131	17.4	204	1	PDGA_RAT	PLATELET-DERIVED GROWT	7.56e-09
25	131	17.4	211	1	PDGA_HUMAN	PLATELET-DERIVED GROWT	7.56e-09
26	130	17.2	226	1	PDGA_XENLA	PLATELET-DERIVED GROWT	1.17e-08
27	91	12.1	411	1	DHE3_VITVI	GLUTAMATE DEHYDROGENAS	7.79e-02
28	91	12.1	493	1	ACHE_HUMAN	ACETYLCHOLINE RECEPTOR	7.79e-02
29	90	11.9	539	1	LI14_CAEEL	LIN-14 PROTEIN.	1.12e-01
30	88	11.7	598	1	CYSJ_SALTY	SULFITE REDUCTASE (NAD	2.27e-01
31	87	11.5	411	1	LYOX_MOUSE	PROTEIN-LYSINE 6-OXIDA	3.23e-01
32	86	11.4	567	1	CCB2_HUMAN	DIHYDROPYRIDINE-SENSIT	4.57e-01
33	84	11.1	916	1	SCRB_LIMPO	BETA SCRUIN.	9.09e-01
34	83	11.0	174	1	YY19_HUMAN	HYPOTHETICAL Y-CHROMOS	1.28e+00
35	83	11.0	308	1	KHSE_BRELA	HOMOSERINE KINASE (EC	1.28e+00
36	83	11.0	393	1	OMPL_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
37	83	11.0	393	1	OMPE_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
38	83	11.0	394	1	OMPM_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
39	83	11.0	396	1	OMPA_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
40	83	11.0	397	1	OMPC_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
41	83	11.0	397	1	OMPN_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
42	83	11.0	397	1	OMPH_CHLTR	MAJOR OUTER MEMBRANE P	1.28e+00
43	83	11.0	399	1	P2X1_RAT	P2X PURINOCEPTOR 1 (AT	1.28e+00
44	83	11.0	491	1	ACHE_BOVIN	ACETYLCHOLINE RECEPTOR	1.28e+00
45	83	11.0	1110	1	VGLM_INSV	M POLYPROTEIN PRECURSO	1.28e+00

ALIGNMENTS

RESULT 1
ID VEGB_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE FACTOR).
GN VEGFB OR VRF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96197355.
RA OLOFSSON B., PAJUSOLA K., KAIPAINEN A., VON EULER G., JOUKOV V.,
RA SAKSELA O., ORPANA A., PETTERSSON R.F., ALITALO K., ERIKSSON U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,
RA WARD L., HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL; U48801; G1234823; -.
DR EMBL; U43369; G1216398; -.
DR MIM; 601398; -.
DR PROSITE; PS00249; PDGF; 1.
KW MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21261 MW; 35EA8904 CRC32;

Query Match 99.3%; Score 749; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 9.02e-157;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:56:46 1998; MasPar time 6.34 Seconds
582.395 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 38.722; Variance 77.276; scale 0.501

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	682	90.5	188	2	JC4680	vascular endothelial	9.95e-114
2	682	90.5	207	2	JC4679	vascular endothelial	9.95e-114
3	256	34.0	232	2	A41551	vascular endothelial	8.21e-29
4	249	33.0	190	2	S52130	vascular endothelial	1.65e-27
5	244	32.4	190	2	A35987	glioma-derived vascul	1.40e-26
6	240	31.8	190	2	B44881	vascular endothelial	7.68e-26
7	240	31.8	190	2	B40080	vascular endothelial	7.68e-26
8	240	31.8	214	2	A44881	vascular endothelial	7.68e-26
9	235	31.2	146	2	S57956	ovine vascular endoth	6.41e-25
10	231	30.6	133	2	B49530	vascular endothelial	3.48e-24
11	227	30.1	120	2	A33787	vascular endothelial	1.88e-23
12	218	28.9	149	2	A41236	placental growth fact	8.17e-22
13	206	27.3	158	2	A56125	placental growth fact	1.19e-19
14	172	22.8	148	2	D49530	16K vascular endothel	1.13e-13
15	166	22.0	419	2	S69207	vascular endothelial	1.20e-12
16	160	21.2	128	2	I51295	vascular endothelial	1.24e-11
17	157	20.8	225	2	S25097	platelet-derived grow	3.96e-11
18	153	20.3	245	1	TVCTSS	platelet-derived grow	1.84e-10
19	152	20.2	241	1	PFMSGB	platelet-derived grow	2.70e-10
20	150	19.9	161	2	I38108	platelet-derived grow	5.79e-10
21	150	19.9	185	2	S58383	hypothetical protein	5.79e-10
22	150	19.9	226	1	TVMVSS	PDGF-related transfor	5.79e-10
23	150	19.9	230	2	A55030	platelet-derived grow	5.79e-10
24	150	19.9	241	1	PFHUG2	platelet-derived grow	5.79e-10
25	150	19.9	271	2	A25669	PDGF-related transfor	5.79e-10
26	138	18.3	166	2	JN0248	platelet-derived grow	5.24e-08
27	138	18.3	198	2	JS0735	platelet-derived grow	5.24e-08
28	133	17.6	63	5	1PDGB2	Platelet-derived grow	3.30e-07
29	133	17.6	66	5	1PDGC2	Platelet-derived grow	3.30e-07
30	133	17.6	68	5	1PDGA2	Platelet-derived grow	3.30e-07
31	131	17.4	196	2	B28964	platelet-derived grow	6.84e-07
32	131	17.4	197	2	S25096	platelet-derived grow	6.84e-07
33	131	17.4	211	1	PFHUG1	platelet-derived grow	6.84e-07
34	130	17.2	200	2	I51551	platelet-derived grow	9.83e-07
35	130	17.2	215	2	S08220	platelet-derived grow	9.83e-07
36	130	17.2	226	2	I51550	platelet-derived grow	9.83e-07
37	128	17.0	196	2	A37359	platelet-derived grow	2.02e-06
38	112	14.9	196	2	A48851	platelet-derived grow	5.56e-04
39	91	12.1	36	2	A60706	vascular endothelial	5.05e-01
40	91	12.1	411	2	S54797	glutamate dehydrogena	5.05e-01
41	91	12.1	493	2	S34775	nicotinic acetylcholi	5.05e-01
42	90	11.9	537	2	B40581	embryonic nuclear pro	6.84e-01
43	90	11.9	539	2	A40581	embryonic nuclear pro	6.84e-01
44	88	11.7	599	2	A34231	sulfite reductase (NA	1.25e+00
45	88	11.7	604	2	A42044	beta subunit of L-typ	1.25e+00

ALIGNMENTS

```
RESULT    1
ENTRY             JC4680     #type complete
TITLE             vascular endothelial growth factor-related factor 167 - mouse
ALTERNATE_NAMES   VRF 167 protein
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              10-May-1996 #sequence_revision 19-Jul-1996 #text_change
                    10-Sep-1997
ACCESSIONS        JC4680
REFERENCE         JC4679
   #authors       Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
                    Nordenskjoeld, M.; Weber, G.; Hayward, N.
   #journal       Biochem. Biophys. Res. Commun. (1996) 220:922-928
   #title         Characterization of the murine VEGF-related factor gene.
   #accession     JC4680
      ##molecule_type mRNA
      ##residues      1-188 ##label TOW
      ##cross-references GB:U43837; NID:g1314335; PID:g1314336
COMMENT     This factor is a mitogen, that is selective for endothelial cells,
            and belongs to a family of growth factor. This transcript is
            differentially spliced to produce two major isoforms, vascular
            endothelial growth factors 167 and VEGF 186.
GENETICS
   #gene          vrf
   #map_position  19
   #introns       137/2
FEATURE
   1-21                #domain signal sequence #status predicted #label SIG\
   22-188              #product vascular endothelial growth factor-related
                         factor #status predicted #label MAT
SUMMARY           #length 188  #molecular-weight 21442  #checksum 5881

  Query Match           90.5%;  Score 682;  DB 2;  Length 188;
  Best Local Similarity  87.0%;  Pred. No. 9.95e-114;
  Matches    87;  Conservative    8;  Mismatches   5;  Indels   0;  Gaps   0;

Db       1 MSPLLRRLLLVALLQLARTQAPVSQFDGPSHQKKVVPWIDVYARATCQPREVVVPLSMEL 60
           |||||||||| |||||| :|||||| |:|:||:|||:|||||:|||||||||||||::||
Qy       1 MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWIDVYTRATCQPREVVVPLTVEL 60

Db      61 MGNVVKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQ 100
           || | ||||||||||||||||||||||||||||||||||||
Qy      61 MGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQ 100


RESULT    2
ENTRY             JC4679     #type complete
TITLE             vascular endothelial growth factor-related factor 186 - mouse
```

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:55:32 1998; MasPar time 4.82 Seconds
339.293 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 28.818; Variance 119.725; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	754	100.0	101	19	W00728	Vascular endothelial	8.29e-64
2	749	99.3	143	19	W00727	Vascular endothelial	2.66e-63
3	749	99.3	188	21	W04829	Fibrosarcoma vascular	2.66e-63
4	749	99.3	188	19	W00726	Vascular endothelial	2.66e-63
5	749	99.3	207	21	W04831	Vascular endothelial	2.66e-63
6	749	99.3	207	19	W00725	Vascular endothelial	2.66e-63
7	682	90.5	133	21	W04828	Vascular endothelial	1.54e-56
8	682	90.5	188	21	W04826	Heart vascular endoth	1.54e-56
9	682	90.5	188	19	W00864	Murine VRF167.	1.54e-56
10	682	90.5	195	21	W04827	Heart vascular endoth	1.54e-56
11	682	90.5	207	21	W04830	Vascular endothelial	1.54e-56
12	682	90.5	207	19	W00863	Murine VRF186.	1.54e-56
13	625	82.9	221	23	W07611	Human vascular endoth	8.38e-51
14	494	65.5	102	21	W04824	Vascular endothelial	1.04e-37
15	268	35.5	595	18	W00595	SAP-GlySer-VEGF165(Gl	1.21e-15
16	266	35.3	377	18	W00586	SAP-AlaMet-VEGF121.	1.88e-15
17	266	35.3	421	18	W00584	SAP-AlaMet-VEGF165.	1.88e-15
18	266	35.3	500	18	W00589	SAP-AlaMet-VEGF121-Gl	1.88e-15
19	266	35.3	506	18	W00588	SAP-AlaMet-VEGF121(Gl	1.88e-15
20	266	35.3	512	18	W00590	SAP-AlaMet-VEGF121(Gl	1.88e-15
21	266	35.3	588	18	W00592	SAP-AlaMet-VEGF165-Gl	1.88e-15
22	266	35.3	594	18	W00591	SAP-AlaMet-VEGF165(Gl	1.88e-15
23	266	35.3	600	18	W00593	SAP-AlaMet-VEGF165(Gl	1.88e-15
24	259	34.4	148	18	R94032	VEGF121 Cys+2.	8.65e-15
25	259	34.4	192	18	R94040	VEGF165 Cys+2.	8.65e-15
26	259	34.4	384	18	R94071	SAP(Gly4Ser)VEGF121.	8.65e-15
27	259	34.4	399	18	W00587	SAP(Gly4Ser)4VEGF121.	8.65e-15
28	259	34.4	428	18	R94072	SAP(Gly4Ser)VEGF165.	8.65e-15
29	259	34.4	443	18	W00585	SAP(Gly4Ser)4VEGF165.	8.65e-15
30	259	34.4	514	18	R94073	SAP(Gly4Ser)VEGF121(G	8.65e-15
31	259	34.4	524	18	W00594	SAP(Gly4Ser)2VEGF121(	8.65e-15
32	259	34.4	598	18	R94074	SAP(Gly4Ser)VEGF165(G	8.65e-15
33	259	34.4	612	18	W00596	SAP(Gly4Ser)2VEGF165(	8.65e-15
34	256	34.0	191	27	W38242	Vascular endothelial	1.66e-14
35	256	34.0	191	16	R91076	Human vascular endoth	1.66e-14
36	256	34.0	191	19	W00724	Vascular endothelial	1.66e-14
37	256	34.0	191	2	R08002	Human vascular endoth	1.66e-14
38	256	34.0	215	18	R94003	VEGF189.	1.66e-14
39	256	34.0	215	16	R91077	Human vascular endoth	1.66e-14
40	256	34.0	215	1	R05102	Human vascular permea	1.66e-14
41	256	34.0	232	18	R94004	VEGF206.	1.66e-14
42	256	34.0	232	16	R91078	Human vascular endoth	1.66e-14
43	256	34.0	461	18	W00583	VEGF165-AlaMet-SAP.	1.66e-14
44	256	34.0	546	27	W38234	VEGF/CPG2 fusion prot	1.66e-14
45	256	34.0	592	27	W38233	VEGF/CPG2 fusion prot	1.66e-14

ALIGNMENTS

RESULT 1
ID W00728 standard; Protein; 101 AA.
AC W00728;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e4.
KW Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;
KW astroglial proliferation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..21
FT /label= Sig_peptide
PN WO9627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI; 96-412774/41.
DR N-PSDB; T33613.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 14; Page 48; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 101 AA;

Query Match 100.0%; Score 754; DB 19; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.29e-64;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 14:00:02 1998; MasPar time 7.25 Seconds
441.000 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 288199 seqs, 31643258 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP
17:NEWU6 18:NEWU7 19:NEWU8 20:NEWU9

Statistics: Mean 28.480; Variance 119.199; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	749	99.3	188	10	US-	Sequence 56, Applicati	1.35e-62
2	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
3	749	99.3	188	10	US-	Sequence 11, Applicati	1.35e-62
4	749	99.3	188	10	US-	Sequence 11, Applicati	1.35e-62
5	749	99.3	188	11	US-	Sequence 57, Applicati	1.35e-62
6	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
7	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
8	749	99.3	188	8	US-	Sequence 11, Applicati	1.35e-62
9	749	99.3	206	12	US-	Sequence 2, Applicatio	1.35e-62
10	749	99.3	207	9	US-	Sequence 15, Applicati	1.35e-62
11	749	99.3	207	9	US-	Sequence 15, Applicati	1.35e-62
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ALIGNMENTS

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CC    Sequence 56, Application US/08671573B
CC     GENERAL INFORMATION:
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Joukov, Vladimir
CC       TITLE OF INVENTION:  Receptor Ligand
CC       NUMBER OF SEQUENCES:  58
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
CC         STREET:  6300 Sears Tower, 233 South Wacker Drive
CC         CITY:  Chicago
CC         STATE:  Illinois
CC         COUNTRY:  United States of America
CC         ZIP:  60606-6402
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/671,573B
CC         FILING DATE:  28-JUN-1996
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/601,132
CC         FILING DATE:  14-FEB-1996
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/585,895
CC         FILING DATE:  12-JAN-1996
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/510,133
CC         FILING DATE:  01-AUG-1995
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Gass, David A.
CC         REGISTRATION NUMBER:  38,153
CC         REFERENCE/DOCKET NUMBER:  28967/33348
CC       TELECOMMUNICATION INFORMATION:
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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:59:37 1998; MasPar time 1.79 Seconds
399.364 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPLLRRLLLAALLQLAPAQ.....CPDDGLECVPTGQHQVRMQT 101

Scoring table: PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 26.807; Variance 113.192; scale 0.237

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	263	34.9	215	3	5219739-22	Patent No. 5219739.	1.34e-15
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19	227	30.1	164	3	5219739-17	Patent No. 5219739.	3.13e-12
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ALIGNMENTS

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CC    Sequence 11, Application US/08469427A
CC    Patent No. 5607918
CC     GENERAL INFORMATION:
CC       APPLICANT:  Eriksson, Ulf
CC       APPLICANT:  Olofsson, Birgitta
CC       APPLICANT:  Alitalo, Kari
CC       APPLICANT:  Pajusola, Katri
CC       TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC       TITLE OF INVENTION:  DNA CODING THEREFOR
CC       NUMBER OF SEQUENCES:  17
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Evenson, McKeown, Edwards & Lenahan
CC         STREET:  1200 G Street, N.W., Suite 700
CC         CITY:  Washington
CC         STATE:  DC
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/469,427A
CC         FILING DATE:  06-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/397,651
CC         FILING DATE:  01-MAR-1995
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Evans, Joseph D
CC         REGISTRATION NUMBER:  26,269
CC         REFERENCE/DOCKET NUMBER:  41979cp2
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (202) 628-8800
CC         TELEFAX:  (202) 628-8844
CC       INFORMATION FOR SEQ ID NO:  11:
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